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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1683
1 atgtttgccaggatgtctga.....aaagtgaaagtggcttctaa 1683
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11:
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SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:

*SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:

*SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:

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*SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:

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*SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:

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*SIDSZ/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*

*SIDSZ/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*

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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMARIE

Result No.	Score	Query Match Length DB	ength	DB	ID	Description
11111				1		
1	1683	100.0	1683	24	AAL45696	Human blood coagul
2	1683	100.0	3008	24	ABN95170	Gene #1668 used to
w	1679.8	99.8	1683	24	AAL45697	Human blood coagul
4	1678.2	99.7	3623	21	AAC76693	Human ORFX ORF2248
S	526.4	31.3	617	21	AAA44763	Human secreted exp
6	242.6	14.4	397	24	ABI99281	Mouse ischaemic co
c <b>7</b>	120.2	7.1	451	22	ABA58323	Human foetal liver
ი 80	120.2	7.1	451	22	AAK06420	Human brain expres
c 9	120.2	7.1	451	22	AAK32096	Human bone marrow

	4.	44	43	42	41	40	35	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21					c 16		14	13	12	c 11	
	7	7	7	7	7	75.4	75.	75.	75.	75.	75	75.	7	75.	7	7	7	78.	78.	79.	84.	85.	86.	87.6	90.	96.			11	11	11	117.	117.	117	120.	120.
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	1068	1068	1068	1068	1068	1068	1068	1068	1068	1068	1068	1065	1065	1047	2100	2097	1620	1689	919	2257	2137	1422	1323	2252	2512	970	117	117	117	117	117	2036	2036	2033	451	451
	14	14	14	14	14	14	14	14	14	14	14	18	18	14	12	12	11	10	18	11	11	8	œ	11	12	15	24	22	22	22	22	24	24	15	24	22
i	AAQ40681	AAQ40679	AAQ40677	AAQ40673	AAQ40671	AAQ40669	AAQ40667	AAQ40660	AAQ40657	AAQ53322	AAQ53320	AAT62606	AAT87456	AAQ40658	AAQ12074	AAQ12071	AAQ00543	AAN91217	AAT90048	AAQ05674	AAQ05675	AAN70991	AAN70992	AAQ05673	AAQ12867	AAQ63945	ABS19403	AA151106	AAK45153	AAK19188	ABA70919	ABL65242	ABN95114	AAQ63951	ABS06863	AAI37947
	tPA-18 cDNA. Synt	CDNA.	CDNA.	CDNA.	CDNA.	CDNA.	CDNA.	6 CDNA. S	1 cDNA.	n truncat	ted	DNA encoding t-PA		tPA-2 cDNA. Synth	٠,	T-PA with -ve char	Vampire bat plasmi	Mutated cDNA codin	Chicken urokinase	v-PA_alpha2. Desm	v-PA_beta. Desmod	Modified tissue pl	Modified tissue pl	v-PA_alpha1. Desm	JM1-229 cell line	$\circ$			Human bone marrow	Human brain expres	ם	Lung cancer relate	_	0		Probe #6633 used t

## ALIGNMENTS

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RESULT 1
AAL45696
26-JUL-2000;
10-OCT-2000;
21-OCT-2000;
12-APR-2001;
                                                                                                                              CDS
                                                                                                                                                                          Human; blood coagulation factor VII activating protease: FSAP; single-chain plasminogen activator; bleeding disorder; haematological; haemostatic; gene; ds.
                                                                                                                                                                                                                                                                       AAL45696 standard; DNA; 1683 BP
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                               Human blood coagulation factor VII activating protease DNA
                                                                                                                                                                                                                                                     AAL45696;
                                                                                                                                                                                                                                  13-JUN-2002
                                                      05-JUL-2001; 2001EP-0115691
                                                                        27-FEB-2002.
                                                                                           EP1182258-A1
         ; 2000DE-1036641.
; 2000DE-1050040.
; 2000DE-1052319.
; 2001DE-1018706.
                                                                                                                                                                                                                                 (first entry)
                                                                                                                    Location/Qualifiers
1.1683
/*tag= a
                                                                                                           /*tag= a
/product= "FSAP"
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Query Match
Best Local Similarity
Matches 1683; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a mutant of the DNA sequence encoding the protease (FSAP) that activates load coagulation factor VII (FVII) and single-chain plasminogen activator, where at least one of the base changes G to C at nucleotide 1177 and G to A at nucleotide 1601 is present. The mutant sequences can be used in the treatment and prevention of bleeding disorders associated with inherited or acquired defects of blood coagulation factors V, VIII, IX, XI, XII, von Willebrand's factor and/or with antibodies against any of these proteins. The present sequence is the human FSAP coding squence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding mutant factor 7 activating protease, useful for diagnosis, treatment and prevention of coagulation disorders, als related protein and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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Nerlich C,
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CAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC
                                                                                                                                                                                                                                                                                                                        GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACAC
                                                                                                                                                                                                                                                                                                                                                                                             GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG
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                                                                           CAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC
                                                                                                                                                    AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC
                                                                                                                                                                      AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Page 15-16; 27pp; German.
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n G;
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 100.0%;
Matches 1683; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                               tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and the method of the invention has hepatotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1668; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2000; 2000US-237054P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene #1668 used to diagnose liver cancer.
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                                                                                                                                                                                                                                                                                                                               Sequence 3008 BP; 791 A; 837 C; 703 G; 677 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENE LOGIC INC.
                                      217
                                                                        121
                                                                                                             157
181 CATGCTGAGAATCCTGACTGGTACTACACTGAGGGACCAAGCTGATCCATGCCAGCCCAAC 240
                                                                                                                                                                               97
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                                                                                                                                                                                                    1 ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60
                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                    GCCTGTGGGGTTCTCCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120
                                                                                                             GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 216
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Pred. No. 0;
0; Mismatches
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Оу	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	dd VQ	Qy Db	Qy Db	Qу Db	Qy bb	Qy Db	Qy Db	Db
1201 1297 1261	1141 1237	1081 1177	1021 1117	961 1057	901 997	841 937	781 877	721 817	661 757	601 697	541 637	481 577	421 517	361 457	301 397	241 337	277
TACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTG	AAGAAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCAC 	GCCCACTGCACCGACATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG	ATGCCCCAGGGCCACTTCTGTGGTGGGGGCCCAATCCACCCCTGCTGGTGGTGCTCACTGCT	ACGGCGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCTGGCTGCCTGACCATCTCC	TGTGGAAAGACTGAGATAGCAGAGAGAGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGC 	GTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCCGGGGTTTGACTCC	GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGAC	GGGGAACACAATTTCTGCAGAAACCCAGATGGGGACGAAAAGCCCTGGTGCTTTATTAAA 7 	CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT 7	TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC 6  ++++++++++++++++++++++++++++++++++++	CAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC	AATGGGGCTACCTGCCGGCATAAGCGGAGATCGAAGTTCACCTGTGCCTGTCCCGAC 5	CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 4	GCCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACAC 4	GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT 3 	CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG 3	
1260 1356 1320	1200 1296	1140 1236	1080 1176	1020 1116	960 1056	900	840 936	780 876	720 816	660 756	600	540	180	120	156	396	36

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RESULT 3
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single-chain
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                                                                                             26-JUL-2000; 2000DE-1036641.
10-OCT-2000; 2000DE-1050040.
21-OCT-2000; 2000DE-1052319.
12-APR-2001; 2001DE-1018706.
                                                                                                                                             05-JUL-2001; 2001EP-0115691
                                                                                                                                                               27-FEB-2002
                                                                                                                                                                                                                                                     Synthetic.
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 New nucleic
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                                                                         (AVET ) AVENTIS BEHRING
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                            2002-270939/32.
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 acid
                                                                                                                                                                                                                                                                                                                     coagulation
                                               Muth-Naumann
                                                                                                                                                                                                                                                                               coagulation factor VII activating protease; plasminogen activator; bleeding disorder; humutant; gene; ds.
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/product= "mutant FSAP"
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mutant factor
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activating
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protease,
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for diagnosis, treatment and related protein and antibodie
  ument and prevention
antibodies -
                           of coagulation disorders,
                             also
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SXCCCCCCCCCXXX German.

The present invention relates to a mutant of the DNA sequence encoding the protease (FSAP) that activates blood coagulation factor VII (FVII) and Single-chain plasminogen activator, where at least one of the base changes G to C at nucleotide 1177 and G to A at nucleotide 1601 is present. The mutant sequences can be used in the treatment and prevention of bleeding disorders associated with inherited or acquired defects of blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's factor and/or with antibodies against any of these proteins. The present sequence is the mutant human FSAP coding squuence.

Sequence 1683 BP; 441 A; 437 C; 435 G; 370 T; 0 other;

Query Match Best Local Matches 1681;

Similarity

99.88;

DB 2; 24;

Length

1683; 0; Gaps

0;

Conservative

0; Mismatches Score 1679.8; Pred. No. 0;

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TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC
                                                                                                            CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG
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                                              CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT
                                                                                                                                                  AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC
                                     CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT
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Human ORFX ORF2248 polynucleotide sequence

SEQ

IJ

NO:4495

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RESULT 4
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ID AAC7
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AC AAC7
XX
AC AAC7
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immunostimulant; thrombolytic; coagulant; vasotropic; antiidabbetic hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hyperte neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A
                                                                                                                                                         cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; mallaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame: ORFX; detection; vulnerary; antipsoriatic; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;
WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nootropic; neuroprotective;
immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertension;
                                                                                                                                                                                                                                                                                                                                                                                      AIDS;
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05-OCT-2000

31-MAR-2000; 2000WO-US08621

31-MAR-1999; 02-APR-1999; 05-APR-1999; 30-MAR-2000; ; 99US-0127607. ; 99US-0127636. ; 99US-0127728. ; 2000US-0540763.

(CURA-) CURAGEN CORP

Shimkets

2000-602362/57 DB; AAB42484.

Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease frame ×

5; Page 3679-3681; 5507pp; English.

CC which represent the human ORFX open reading frames 1 to 3161. The ORFX CS sequences have activities such as: cytostatic; neuropic; vulnerary; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; CC immunostimulant; cardiant; thrombolytic; coagulant; vascroptc; (CC antidiabetic; hypotensive; dermatological; immunosuppressant; cardiabetic; hypotensive; dermatological; immunosuppressive; CC antityoid; and antianaemic. The sequences can be used for determining CC the presence of or predisposition to, or preventing or treating CC pathological conditions associated with an ORFX-associated disorder. The colleic acids can be used to express ORFX proteins in gene therapy; CC proliferative disorders, neurodegenerative disorders, settlitus, the proteins and nucleic acids may be used to treat cancers, CC proliferative disorders, neurodegenerative disorders, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, vital, CC barterial or fungal infection, malaria, autoimmune disorders, asthma, CC capulation; to inhibit thrombosis; and as a contraceptive.

3623 BP; 848 A; 1005 C; 930 G; 840 T; 0 other; Qy

Вb

Qy В 2 В QY Дb Qy В ρy В δÃ В Qy рь Qy рь Š рь δÃ B 20 В δÕ рь Q В Ş B Ş

DЬ

Query Match Best Local s Matches 1680 Similarity Conservative 99.7%; Score 1678.2; Pred. No. 0; 0; Mismatches 0; DB ω,. 21; Indels 3623; 0; Gaps 0,

ATGITTGCCAGGATGICTGATCTCCATGITTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anticorvulant; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the sESTs. Proteins encoded by the sESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Nazheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammator, disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAAA5926 to AAA45931 represent linker variants which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemotactic; proliferative; immunomodulatory; haematopoietic;
chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 549; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-317938/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEMY ) GENETICS INST INC
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                                                                                                                                              CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG
                                                                                                                                                                                                   CACGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC
                                                                                                                                                                                                                       CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC
                  GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACAC
                                                                         GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT
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GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 526.4;
Pred. No. 2.8e
0; Mismatches
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                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                       ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABH59202 to ABH59912, encoding the protein sequences in ABB57020 to ABH57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI59913 and ABI59914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                               1363 ACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAAC 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2002
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                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABI99281 standard; cDNA; 397
Ishikawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
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                                                                                                                                                                             Local Similarity 84. es 272; Conservative
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                                                         ACAGAAACAGGGGAAGGGTCCCGCCAGCTCCTGGATGCTAAAGTCAAGCTAAATCGCTAAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Page 351-352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ischaemia; compressive ischaemia;
astic ischaemia; ischaemic condition
                                                                                                                                                                                                                                                                                                        397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention describes a method for examining
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                                                                                                                                                                                                                                                                                                    BP; 103 A; 105 C; 111 G; 78 T; 0 other;
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                                                                                                                                                                             Score 242.6; DB 24;
Pred. No. 5.2e-60;
0; Mismatches 49;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA58323 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA58323;
                                                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; foetal liver; gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                       analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157277-A2
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  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGAGAAGGATGGAACTTACTACGTCTACGGGATTGTAAGCTGGGGCCAGGAATGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGAACCTTCAGAAGCCCGGATCAGACACCTGCCAGGGTGACTCGGGGGGCCCTCTAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACAGGGAGGCTGGCCTCTGA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAAGCCAGGAGTCTACACTCAAGTCACCAAGTTCCTGAATTGGATAAAGACCACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAGGCCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATC
                                                   of the invention.

The sequence data for this patent did not form part of each specification, but was obtained in electronic format wipo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      foetal liver single
                                                                                                                                                                                                                                                                                                                    1; SEQ ID NO 6628; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful
zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC
     451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-02346359.
; 2000US-0236359.
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  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DK,
     116
  A; 102 C; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
     G; 106 T; 0 other;
                                                                                  directly
                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1662
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Query Match Best Local Similarity

7.1**%**; 97.6**%**;

Score

No. 120.2;

1.8e-24;

DB 22; Length 451;

Qy 멍

0;

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RESULT 8
AAK06420/c
ID AAK064
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         Query Match
Best Local :
Matches
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26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
21-SEP-2000;
27-SEP-2000;
27-SEP-2000;
                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                           Single
brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray; Alzheimer's disease;
epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK06420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK06420 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                            WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-2001
                                          Sequence 451
                                                                                                                                                                                                                                                                            04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331
                                                                invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGAGTCCTCCCTACTACCGCTGTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGAGTTCCTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAAG
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                                                                                                                                                                                                            2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122;
                                                                                                                                                                                exon nucleic acid
                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS
         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448
                                                                                                                                                                                                                                 Hanzel
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                                                                                                                                                      SEQ ID NO: 6411; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                         2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
Conservative
                                           BP; 116 A; 102
                                                                                                                                                                                                                                                                                                                                                                  2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                                                                                                                                                                                                                                DK,
          7.18;
97.68;
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                                                                                                                                                                                      probes
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0;
                                           C; 127 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
          Score 120.2; DB 2
Pred. No. 1.8e-24;
                                                                                                                                                                                                                                   Rank
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 Mismatches
                                                                                                                                                                                       for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probe SEQ
                                                                                                                                                                                                                                    DR;
                                            106
                                            T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO:
                      22;
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  Indels
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                        Length
                        451;
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 Gaps
                                                                                                              samples
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331 444 391 384

CCAAG CCAAG

448 327

AAK32096;

AAK32096 standard;

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bone marrow expressed single
                                                                                                                                                                                                                                                                                                                                                      Sequence 451 BP; 116 A; 102 C; 127 G; 106 T; 0 other;
                                                                                                                                                                                            TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCCGGGGCCAATGTCTCATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGAGTCCTCCCTACCGCTGTGTCTGTAAACACCCTTACAAGGTCCCAGCTGCTC
                                                                                                                  CCAGAGTCCTCCCTACTACCGCTGTGTGTAAACACCCTTACACAGGTCCCAGCTGCTC
                                                                                                                                                               TCCTACAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes useful zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO: 6653; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
                                                                                                                                                                                                                                                                               7.1%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                        Score 120.2; DB 2
Pred. No. 1.8e-24;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                    22; Length 451;
                                                                                                                                                                                                                                                          Ψ
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                          Gaps
                                                                                                                  443
                                                                                                                                                               392
                                                                                                                                                                                                           383
                                                                                                                                                                                                                                                             0
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AAI37947/C
ID AAI37
XX AAI37
AC AAI37
XX Probe
XW Probe
KW Probe
KW Genet
XX U020C

ABS06863/c
ID ABS068
XX
AC ABS068
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                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                 Вþ
                                                                                              RESULT
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Best Local Sim
Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI37947 standard;
  ABS06863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID No 6633; 654pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 451 BP; 116 A; 102 C; 127 G; 106 T; 0 other;
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                                               ABS06863 standard;
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                                                                                                                                                                                                                                                                                                                                                      TCCTACAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC
                                                                                                                                                                                                                                                                                                                                                                             TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC 383
                                                                                                                                                                                                                                                          CCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACACCCCTTACACAGGTCCCAGCTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                               DNA; 451 BP
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97.68;
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Pred. No. 1.8e-24;
0; Mismatches 3
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RESULT 9
AAK32096/c
ID AAK320
XX AAK320
XX O6-NOV
XX DF Human
XX Human
XX Human
XX Homo \$
XX WO2001
XX O9-AUC
XX O9-

04-FEB-2000; 26-MAY-2000; 30-JUN-2000; 03-AUG-2000; 21-SEP-2000; 27-SEP-2000; 04-OCT-2000;

30-JAN-2001; 09-AUG-2001. WO200157276-A2 Homo sapiens

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CCAAG

448

Query Match Best Local S Matches 122

al Similarity 122; Conserv

o f

Example 4;

WPI; 2001-488900/53.

(MOLE-)

SG,

Hanzel

DK,

19-AUG-2002 (first entry)

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CC probes; the novel set of probes which hybridise at high stringency to a connected are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a connected acid expressed in the human lung; measuring gene expression in a consection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with caracteristic acids derived from human lung comprising (a) contacting the array with caracteristic expression in a contacting the array with caracteristic exids derived from human lung communication of detectably bound to each probe of contentifying exons in a eukaryotic genome, comprising confidentifying exons in a eukaryotic genome, comprising confidentically predicting at least one exon from genomic sequences confidentifying exons in a eukaryote lung mRNA, to a single exon probe, captured nucleic acids from eukaryote lung mRNA, to a single exon probe, comprising (a) identifying exons from genomic sequence by the method confidential to the predicted exon, the probe is included comprising (a) identifying exons from genomic sequence by the method confidential to the expression of each of the exons in several common success to a single exon probe with the exon with the exon probe indicates that confidential by probe with the exon, where a common pattern of confidential probes assigned to a single gene; a peptide comprising one confidential to the sassigned to a single gene; a peptide comprising one confidential to the exons in the tissues and/or cell types indicates that the exon should be assigned to a single gene; a peptide comprising one confidential to the confidential to the confidential to the exons in the confidential to the exons the confidential to the exons that the exon probe in the exons in the confidential to the exons the probe of the exons the probe of the exons that the exon probe in the exons the problem to the
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30-JUN-2000;
03-AUG-2000;
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of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples \mbox{-}
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2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
2000US-236359P.
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               sarcoidosis, pulmonary
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                                                                  pulmonary
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RESULT 12
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ID AAQ63
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Best Local
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                                                                                                                                                                                                                                                                                                                         05-NOV-1992;
20-NOV-1992;
20-NOV-1992;
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                                        Hepatocyte growth factor converting protease and precursor and gene encoding them - for producing active two chain HGF from
                                                                                                                                                                               Kitamura N,
Yamada K;
                                                                                                                                                                                                                                                   (SHIM/)
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                    inactive single chain
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                                                                                                                1994-152921/19
DB; AAR53962.
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122; Conser
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MITSUBISHI KASEI CORP
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92JP-0312234.
92JP-0312242.
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/product= Hepatocyte growth factor
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97.6%;
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                                                                                                                                                     AAGTACATCCCGTACACCCTGTACTCGGTGTTCAACCCCAGCGACCAC---GACCTCGTC
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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cyvostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug efficacy and drug metabolism.

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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcin adenocarcinoma;

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2000US-209473P.
2000US-209531313P.
2000US-234609P.
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TGGTGCTTTATTAAAGTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCC
                                              GAAACCCATGGGATTGGGGAACACAATTTCTGCAGAAACCCCAGATGCGGACGAAAAGCCC
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GACTGGATCAACGACCGGAT
                           AATTGGATCAAAGCCACCAT
                                                                                                          GGCCTGGAGTGTGGG-----AAGAGGCCAGGGTCTACACCCCAAGTTACCAAATTCCTG
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Search completed: March 6, Job time: 353.5 secs
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26 MAY 2000;
30 JUN 2000;
37 AUG 2000;
21 SEP 2000;
27 SEP 2000;
04 OCT 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \mbox{\it Human genome-derived} single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 117 BP; 24 A; 24 C; 40 G; 29 T; 0 other;
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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435.2	435.4	437.8	447.2	451.6	698.2	
25.9	25.9	26.0	26.6	. 26.8	41.5	Query Match Length DB ID
570	751	674	802	592	891	Length DB
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вм508620	BI148082	AA217892	BG972579	BE032018	BI761782	ID
BM508620 ii37h03.y	BI148082 602912432	AA217892 mv54b08.r	BG972579 602841165	BE032018 130809 MA	BI761782 603046775	Description

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## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL RESULT 1 BI761782 LOCUS KEYWORDS SOURCE FEATURES COMMENT ACCESSION DEFINITION VERSION ORGANISM source L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Capabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1467 row: e column: 19
High quality sequence stop: 839.
Location/Qualifiers
rce
1. 891 Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 891)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) EST mRNA sequence. BI761782 603046775F1 NIH\_MGC\_116 BI761782.1 GI:15753360 891 bp mRNA linear EST 25-SEP-2001 Homo sapiens cDNA clone IMAGE:5187066 5',

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BASE COUNT
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                       GGATTGGGGAA - - CACAATTTCTGCAG - AAACCCCAGATGCGGACG - AAAAGCCCTGGTGC
                                                                CCAAGCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGGATGCTTGAAAACCCATG
                                                                                                        CC-ACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGG---ATGCTGAAACCCATG
                                                                                                                                                     TCTTACCGAGGGAAAATGAATAGGACAGTCAAACCAGCATGCGTGCCTTTACTGGAACTC
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/db_xref="taxon:9606"
41.5%;
97.2%;
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Sus scrofa
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Plate: 69 row: K column: 12
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases ov 0.980904 e. Vector identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal
PO Box 166, Clay Center, N
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST discovery in swine 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Design and use of two pooled tissue normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stone, R.T., Heaton, M.P., and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                   note="Vector: pCMV SPORT6; Site_1: NotI; Site_2:
Library made from pooled tissue from day 11, 13, 1
and 30 embryos."
174 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
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2 c 174 g
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0; Mismatches 69;
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Query Match
Best Local S
Matches 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 802)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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B0972579 NCI_CGAP_Kid14 Mus
5', mRNA sequence.
B0972579
                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
Plate: LLAM10967 row: a column: 17
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Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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  Similarity 77.
80; Conservative
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                                                                                                                   211
                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop:
                                                                                                    /organism="Mus musculus"
/organism="FVB/N"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="ImAGE:4973384"
/clone=1ib="NCI_CGAP_Kid14"
/clone_1ib="NCI_CGAP_Kid14"
/lab_host="D110B_(T1_phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Note="Site_2: Sall; Cloned unidirectionally. primer: Olice Site_2: Sall; Cloned unidirectionally. primer: Olice Sall; Cloned unidirectionally. primer: Olice Site_2: Sall; Cloned unidirectionally. primer: Olice Sall; Cloned unidirectiona
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                   26.6%;
77.7%;
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Score 447.2;
Pred. No. 4.6e
0; Mismatches
    0;
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musculus
2; DB 13;
1.6e-116;
nes 158;
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                        Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostom1; Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus. 1 to 674)

1 (Dases 1 to 674)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., "Lennon,G., Soares,B., Wilson,R. and"
  Theising, B., Wylie, T., Lennon, G., Waterston, R.
                                                                                                                                                                                   Mus musculus
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                                                                  AA217892 674 bp mRNA linear EST (mv54b08.rl Soares mouse 3NWE12 5 Mus musculus cDNA clone IMAGE.658839 5' similar to TR:G1345398 G1345398 HGF ACTIV
                    PROTEIN. ;, mRNA sequence. AA217892
GI:1826875
                                                                                HGF ACTIVATOR LIKE
                                                                                                                                 EST 06-FEB-1997
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               1121 TGCTAGGGGACCAGGACCTGAAGAAAGAAGTTTCATGAGCAGAGCTTTAGGGTGGAGA 1180
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                                                                 1061 CCTGCTGGGTGCTCACTGCTGCCCCACTGCACCATAAAAACCAGCAGCATCTAAAGGTGG
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                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                              CGCTGCCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGGGGCGTGATCCACC
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                                                                                                            CACTGCCGTTGACCACCTCCATGCCCCAAGGCCACTTCTGTGGGGGGGCGCCCTGATCCACC
                                                                                                                                                                           TCTACGGGGGCTTTAAGAGCACAGCAGGCAAGCACCCGTGGCAGGTGTCCCTGCAGACCT
                                              CCTGCTGGGTGCTCACTGCAGCCCACTGTACCGACATAAACACCAAGCATCTAAAAGTTG
                                                                                                                                                                                                        TCTATGGAGGCTTTAAGAGCACGGGGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCT 1000
                                                                                                                                                                                                                                                                                                       CAGTCTGTCCAGTGCCTGACACCCCTAACCCAGTGGAAAGCCTTCTGGAGCCTGTGATGG
                                                                                                                                                                                                                                                                                                                                                                     AACCCTGGTGTTTCGTCAAGGTGAACAGTGAGAAGGTGAAATGGGAATACTGTGATGTCA 120
                                                                                                                                                                                                                                         AGCTGCCAGGGTTCGAGTCCTGCGGGAAGACGGAGGTAGCTGAACACGCAGTCAAGCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL
IMAGE Consortium (info@lmage.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI MOU
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rossible reversed clone: similarity on wrong Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares mouse 3NME12
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:658839"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.0%;
78.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 437.8; DB 9;
Pred. No. 2e-113;
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147;
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62 CATTGGGCTCTCACTGATGTCCTTCATTGCGCCCCCAGACCCAGATTGGACCCCCGATGA 121
                 63 CTGTGGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGACCA 122
                                                                                       4 TTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACAGC- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATATTCAAGTACAGCCACTACAATGAAAGAGATGAGATTCCCCCACAATGATATTGCAT 1240
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                                                                    TTTGTCAGGATGTTGGTGTTCCGTGTCCTGCTAATCGCCCTGGTGGGGAAGTCAGTG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTCAAGTTAAAGCCAGTGGGTGGTCACTGTGCTCTGGAATCCAGATATGTGAAGACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 751)
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                                                                                                                                                                                                                                  188
                                                                                                                                              Conservative
                                                                                                                                                                                                                 /strain="FVB/N"
/db xref="taxon:10090"
/dlone="IMAGE:5053663"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pcMv-SPORT6; Site_1: NotI;
/note="Organ: liver; Vector: pcMv-SPORT6; Site_1: NotI;
/site_2: Sall: Cloned unddirectionally Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
88 a 221 c 188 g 154 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 747.
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                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus
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IMAGE consortium

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RESULT 6
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                                                                                                                                                          Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; 1 (Dases 1 to 570)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BMS08620 570 bp mRNA linear EST 12-MAR-2002 ii37h03.yl melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus muscullus cDNA clone IMAGE:5944156 5' similar to TR:Q14520 Q14520 HGF ACTIVATOR LIKE PROTEIN. ;, mRNA sequence.
                    Contact: Douglas Melton, Klaus H. Kaestner
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
                                                                                                                   Unpublished (2000)
Other_ESTs: ii37h03.x1
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                                                                                           Kaestner, & Hiroshi
                  Institute
Divinity Ave, Cambridge
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                                                                                                                                                                                                                                                                                                                                                    AGCTAATCGCTAACCCTTTGTGCAACTCCCGACAACTCTATGACCACACCATCGATGAC
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AGTATCATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCT
                                                                                                                   TCTGGCTGGGGTGTTACAGAAACAGGGGAAGGGTCCCGCCAGCTCCTGGATGCTAAAGTC
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Library was constructed by Dr. Douglas Melton DNA sequencing by
Washington University Genome Sequencing Center For information
obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (brown@fas.harvard.edu) MGI:2007028 This sequence now available from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for clone orders contact: inf
Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). cDN/was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on Solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,
adult, mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I;
libraries representing EI0.5/12.5 pancreatic bud, E16.
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/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5944156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Both for embryonic & newborn, male for adult and
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KEYWORDS
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ORGANISM
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                      164 GACTATTACTACAGCTATGAGCAGTCCAGCCCAGACGAAGACCCCAGTGTCACGCAGACC
                                                                   121 CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACC 180
                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                    GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120
                                                                                                                                                                                                                              ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60
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                                                                                                                GTCATGGGGCTCTCACTGATGTCCTTCATTGCGCCCCCAGACCCAGATNGGACCCCCGAT
                                                                                                                                                                                                     ATATTTGTCAGGATGTAGGTGTTCCGTGTCCTGCTGCTAATCGCCCTGGTGGGGAAGTCA 103
                                                                                                                                                                                                                                                                                                  529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae; Mus 1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602113411F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:4241642 5', mRNA sequence.
BF788188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D
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/clone="IMAGE:4241642"
/clone=in="NGI_CGAP_Kid14"
/clone=in="NGI_CGAP_Kid14"
/lab host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; cloned unidirectionally primer: Oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 275 c 253 g 162 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   24.7%;
75.9%;
                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                             Score 416.4; DB 12;
Pred. No. 3e-107;
0; Mismatches 162;
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                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lead to the county of the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11328 row: a column: 12
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602980841F1 NCI_CGAP_Li9 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 791)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                        quality sequence stop:
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="ftaxon:10090"
/clone="IMAGE:5133587"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DHIUB (Tl phage resistant)"
/note="Organ: liver: Vector: pCMV-SPORT
                                                                                                                                                                                 Location/Qualifiers
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Rodentia; Sciurognathi; Muridae;
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     pCMV-SPORT6;
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637

577 540 517 480 457 420 397 360 337 300 277

Euteleostomi; Murinae;

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REFERENCE AUTHORS

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QyDЪ

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mx10b10.rl
similar to
                                                                                                              sequence.
AA237499
AA237499.1
Mus musculus
Eukaryota; Metazoa; Chordata;
Eukheria; Rodentia;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 546)
                                                                           house mouse
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234 c 194 g 161 t
                                                                                                                                                              546 bp
Soares mouse NML Mus
TR:G1345398 G1345398
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Pred. No. 1.
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                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                  musculus cDNA clone IMAGE:6797 HGF ACTIVATOR LIKE PROTEIN. ;,
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                                                                                                                                                                                 EST 03-MAR-1997
IMAGE:679771 5'
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                             64 GCAGTCAAGCGTATCTACGGGGGCTTTAAGAGCACAGCAGGCAAGCACCCGTGGCAGGTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GAGCCTGTGATGGAGCTGCCAGGGTTCGAGTCCTGAGGGAAGACGGAGGTAGCTGAACAC
                                                                                                          TTTAGGGTGGAGAAGATATTCAAGTACAGCCACTACAATGAAAGAAGAGATGAGATTCCCCAC
                                                                                                                                                                                     CATCTAAAAGTTGTACTAGGGGATCAGGACCTGAAGAAGACAGAATCCCATGAACAGACC
                                                                                                                                                                                                          CATCTAAAGGTGGTGCTAGGGGACCAGGACCTGAAGAAGAAGAAGAATTTCATGAGCAGAGC 1167
                                                                                                                                                                                                                                                                                   GCGCTGATCCACCCCTGCTGGTGCTCACTGCTGCCCACTGCACCGACATAAAAACCAGA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGATCAAGAGAATCTATGGAGGCTTTTAAGAGCACGGGGGGGCAAGCACCCATGGCAGGGG 987
  AATGATATTGCATTGCTCAAGTTAAAGCCAGTGGATGGTCACTGTGCTCTAGAATCCAAA 128
                                                                                                                                                                                                                                                              GCCCTGATCCACCCCTGCTGGGTGCTCACTGCAGCCCACTGTACCGACATAAACACCAAG
                                                                                                                                                                                                                                                                                                                                       TCCCTGCAGACCTCACTGCCGTTGACCACCTCCATGCCCCAAGGCCACTTCTGTGGGGGC 183
                                                                                                                                                                                                                                                                                                                                                                          TCCCTCCAGTCCTCGCTGCCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGG 1047
                                     AATGACATTGCTTTGCTCAAGTTAAAGCCAGTGGGTGGTCACTGTGCTCTGGAATCCAGA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Possible reversed clone: similarity on wrong
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 405.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

White the manner of the massin-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL ; contact the LMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:419475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo."
a 142 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:679771"
/clone_lib="Soares mouse NML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 395.8; DB 9;
Pred. No. 1.7e-101;
0; Mismatches 92;
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546;

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0; Gaps

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QΥ В Qγ DЪ õ DЬ δÃ 밁 40 В δõ

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KEYWORDS

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363

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JOURNAL
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AUTHORS
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AV601564
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Best Local :
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                           544
181
                                                                                      107
                                                                                                               61 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120
                                                                                                                                            47 ATGTTTGCCAGAATGTCTGATCTCCATGTTCTGCTGTTAATGGTTCTGGCGGGAAAGACA 106
                                                                                                                                                            1 ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGTGAAGACTGTATGTTTGCCCCAGCGACCCCTTTCCCTCTGGAACTGAGTGCCACATC
CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG 546
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                                                                                    GCCTTCGGGCTCTCCCTGCTGTCTTTCTCACAGAGCCGGACCCAGATTGGACTCCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGGCTGGGGTGTTACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTC 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV601564
AV601564 Bos tauru
5', mRNA sequence.
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AV601564.1 GI:9723884
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21570554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Sugimoto, Y Establishment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; F
1 (bases 1 to 608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          poly(A) tail-removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                            148
                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone was obtained from a polyA-deleted
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lishment of a high throughput EST sequencing syst
N) tail-removed cDNA libraries and determination
                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/organism="Bos taurus"
/obaxref="taxxon:9913"
/clone_lib="Bos taurus kidney fe
/tissue_type="kidney"
/dev_stage="fetus"
/lab_host="DH10B"
/note="Vector: pZL1; Site_1: Sal
was deleted from a Not1 site"
8 a 171 c 151 g 135 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pass sequencing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                   23.3%;
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                                                                                                                                                                                                    0;
                                                                                                                                                                                                   Score 392.6; DB 10;
Pred. No. 1.5e-100;
0; Mismatches 97;
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y fetus Bos taurus
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s cDNA clone
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tion of 36,000
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SOURCE
ORGANISM
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δ 밁 γç В QYВ Qy ORIGIN

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Query Match 23.3
Best Local Similarity 73.1
Matches 532; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 480
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602105493F1 NCI_CGAP_Kid14 Mus
5', mRNA sequence.
BF780971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cnNA library procurent:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9812 row: i column: 23
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                   // Strain="FVB/N"

/Strain="FVB/N"

/Gb_xref="taxon:10090"

/Clone="InMc:4223710"

/Clone="lib="NOI_CGAP_Kld14"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: kldney; Vector: pCMV-SPORT6; Site_1: NotI;

/note="Organ: kldney; Vectorinally. Primer: Oligo dT.

Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library. | "

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Ism Mus musculus

Eukaryota; Metazoa; Chordata; Crania...

Mammalia; Butheria; Rodentia; Sciurognathi; Mi
2NCE 1 (bases 1 to 682)

HORS NIH-MGC http://mgc.nci.nih.gov/.

RLE National Institutes of Health, Mammalian Gen

MENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
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High quality sequence stop: 682
Location/Qualifiers
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/clone_lib="NCI_CGAP_Li9"
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/note="Organ: liver; Vector: pCMV-SpORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer: Oli Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 206 c 169 g 141 t
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/strain="FVB/N"
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Best Local S
Matches 478
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               672 GCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCCATGGGATTGGGGAACACAA 731
                                                                                                                                                                               552 GAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTACTCTTACCGAGG
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                                                                                                                  612 GAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCCCACCTCCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 372 ATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACACCCCTTACACAGG 431
                                                                            259 CAAAGTGAGTAAGACAGTCAACCAGAACCCATGCCTTTACTGGAACTCCCACCTCCTCTT 318
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les 478; Conservative
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GCAGGAGACTTATAACATGTTTATGGAGGATGCAGAGACCCACGGGATCGCAGAGCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: ggapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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602112402F1 NCI_CGAP_Kid14 Mus n
5', mRNA sequence.
Be785781 GI:12090817
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Mammalia; Eutheria; Rodentia; Sciurognathi; Mu
I (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Mus musculus
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/clone_lib="NCI_CGAP_Kid14"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (TI_phage-resistant)"
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a 269 c 237 g 185 t
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/strain="FVB/N"
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Pred. No. 3.5e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    912 TGAGATAGCAGAGAGGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGCACGGCGGCA 970
                                           124
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  CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACC
                                           GTCATTGGGCTCTCACTGATGTCCTTCATTGCGCCCCAGACCCAGANTGGACCCCCGAT 183
                                                                                    GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120
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                                                                                                                         ATATTTGTCAGGATGTTGGTGTTCCGTGTCCTGCTGCTAATCGCCCTGGTGGGGAAGTCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9533 row: g column: 01
High quality sequence stop: 692.
Location/Qualifiers
1 g60
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Jeffrey E. Green, M.D.
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Contact: Robert St
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/clone="InAGE:4196376"
/clone=Lib="NCI_CGAP_Li9"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORR6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer: Oli
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
a 278 c 260 g 172 t l others
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76.5%;
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Pred. No. 1.1e-94;
0; Mismatches 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT
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                                                                                                                                                                             Unpublished (1999)
Contact: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schwer,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 654)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW475402 654 bp mRNA linear EST 24-FEB-
un65h07.yl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:2503549 5' similar to TR:Q14520 Q14520 HGF ACTIVATOR LIKE
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                                                                                                                MGI:1018401
                                                                              primer: custom primer used
h quality sequence stop: 48
                                                                                                                             clone is available royalty-free through LLNL; E.Consortium (info@image.llnl.gov) for further
                                                                                                                                                                  mouseest@watson.wustl.edu
/strain="C57BL"
/db_xref="taxon:10090"
                             /organism="Mus musculus"
                                                             Location/Qualifiers
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                                                                              482
                                                                                                                                             LLNL ;
                                                                                                                                                                                                                 MO 63108,
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Job time: 2189.5 secs
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TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCT 647
                                                       CAGGTATAGGGGAAATTCTGTGACATAAGTGCGGACGACTGGTATGTCGGTGATGGCTAC
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3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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Sequence 5, Appli
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                          US-08-148-910-14
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INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 2033 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE: ORGANISM: human IMMEDIATE SOURCE: LIBRARY: pre-made Lambda phage Library, LIBRARY: human liver(49, male) cDNA Library STO8-148-910-14	MEDLUM TYPE: 500 kb Storage COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/148,910 FILING DATE: No. 546593ember 5, 1993 CLASSIFICATION DATA: APPLICATION MUMBER: US/08/148,910 FILING DATE: No. 546593ember 5, 1993 CLASSIFICATION DATA: APPLICATION NUMBER: JT. FILING DATE: FATORNEY/AGENT INFORMATION: NAME: WAITEN M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECHMUNICATION INFORMATION: TELEPHONE: 202-371-8856 TELEPHONE: 202-371-8856 TELEPAX: 202-371-8856	UESULT 1  S-08-148-910-14  Sequence 14, Application US/08148910  Patent No. 5466593  GENERAL INFORMATION:  TITLE OF INVEWTION: No. 5466593el Protein and NUMBER OF SEQUENCES: 14  CORRESPONDENCE ADDRESS:  ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700  CITY: Washington STATE: D.C.  COUNTRY: U.S.A.  ZIP: 20005  COMPUTER READABLE FORM:  MEDIUM TYPE: Diskette, 5.25 inch,	28 73.8 4.4 1163 4 US-09-410-882-5 29 73.8 4.4 1170 2 US-08-811-949-64 30 73.8 4.4 1314 2 US-08-811-949-66 31 73.8 4.4 1314 2 US-08-811-949-50 32 73.8 4.4 1314 2 US-08-811-949-56 34 73.8 4.4 1314 2 US-08-811-949-62 35 73.8 4.4 1738 6 5200340-1 36 73.8 4.4 1974 2 US-08-814-412-10 37 73.8 4.4 1974 2 US-08-814-949-38 38 73.8 4.4 2101 2 US-08-814-949-38 39 73.8 4.4 2101 2 US-08-811-949-38 40 73.8 4.4 2162 1 US-08-119-512-3 41 73.8 4.4 2162 1 US-08-488-0158-3 41 73.8 4.4 2162 1 US-08-488-0158-3 42 67.8 4.0 2494 5200340-5 43 67.8 4.0 2494 5520340-5 43 66.4 3.9 1233 1 US-08-254-922-1
(Stratagene)		Gene Encoding Said Protein	Sequence 5, Appli Sequence 64, Appl Sequence 50, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 62, Appl Patent No. 5200340 Sequence 10, Appl Sequence 31, Appli Sequence 32, Appli Sequence 33, Appli Sequence 25, Appli Sequence 35, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 38, Appli Sequence 39, Appli Sequence 31, Appli Sequence 31, Appli

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AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCT 1527
                                                             TGGGGCCACTTGGATGAGAACGTGAGCGGCTACTCCAGCTCCCTGCGGGAGGCCCTGGTC
                                                                                                                                              TGGGG-----TGTTACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTC
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                                    CCCCTGGTCGCCGACCACAAGTGCAGCAGCCCTGAGGTCTACGGCGCCGACATCAGCCCC
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Patent No. 5
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NAME: Warren M. Cheek, J.
REGISTRATION NUMBER: 33,
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APPLICATION NUMBER: 08/148,910
FILING DATE: No. 5677164ember
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: 500 Kb Storage
MEDIUM TYPE: 1BM Compatible
COMPUTER: 1BM Compatible
OPERATING SYSTEM: MS-DOS
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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JRRENT AFFLICTION NUMBER: US/US/APPLICATION NUMBER: US/US/FILING DATE: May 24, 1995
                                                                                                                                  LIBRARY: Pre-made Lambda phage Library,
LIBRARY: human liver(49, male) cDNA Library (Stratagene
                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                       TYPE: nucleic acid
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CITY: Washington
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                                                            al Similarity
607; Conserv
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805 Fifteenth Street, N.W., #700
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/ENTION: No. 5677164el |
EQUENCES: 14
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                                                         Score 117.6; DB 1;
Pred. No. 6.8e-25;
0; Mismatches 559;
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                                                                                      DB 1;
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                                                                                      Length 2033;
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                      CCCCTGGTCGCCGACCACGAGTGCAGCAGCCCTGAGGTCTACGGCGCCGACATCAGCCCC
                                                                                                                                                                                       GTGTGCTTGCCTGAT---
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                                                                                                            AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCCAGGGTGACTCT
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GGGGGGCCCCTGCCGAGAAGAACGGCGTGGCTTACCTCTACGGCATCATCAGCTGG
                                                                                 AACATGCTCTGTGCCGGCTACTT - - - CGACTGCAAGTCCGACGCCTGCCAGGGGGACTCA
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RESULT 3
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Best Local S
Matches 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
COMPUTER READABLE: FORM:
MEDIUM TYPE: Diskette, 5.25 in
MEDIUM TYPE: 500 kb Storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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1123 CTAGGGGACCAGGACCTGAAGAAGAAGAAGTTTCATGAGCAGAGCTTTAGGGTGGAGAAG 1182
                                                                             1069
                                                                                                                              1009 CTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGGGGCGCTGATCCACCCCTGCTGG 1068
                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Takeshi
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Warren M. Cheek, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                               261
                                                                                                           201 CTGGCCGCCATCTACATCGGGGACAGCTTCTGCGCCCGGGAGCCTGGTCCACACCTGCTGG 260
                                                                                                                                                                        Local Sir
hes 359;
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SOFTWARE: Wordpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 805 Fift
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202-371-8856
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/148, FILING DATE: No. 5466593ember
                                                                                                                                                                                                                                                      LIBRARY:
                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                             GTGGTGTCGGCCGCCCACTGCTTCTCCCACAGCCCCCCAGGGACAGCGTCTCCGTGGTG
                                                                           GTGCTCACTGCCCACTGCACCGACATAAAAACCAGACA-----TCTAAAGGTGGTG 1122
                                                                                                                                                                                                                                                                                                                                                                            H: 970 base pairs
                                                                                                                                                                                       Similarity
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805 Fifteenth Street, N.W.,
                                                                                                                                                                                                                                                    Pre-made Lambda phage Library, human liver (49, male) cDNA Library (Stratagene)
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53.0%;
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No. 5466593el Protein
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                                                                                                                                                                        0;
                                                                                                                                                                       Score 96.2; DB 1;
Pred. No. 1e-18;
0; Mismatches 288
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US-08-448-937A-3
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                                                                                                                                                                                                         MEDIUM TYPE: 500 Kb Storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/4
FILING DATE: May 24, 1995
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                                                           APPLICATION NUMBER: 08/148,910
FILING DATE: NO. 5677164ember
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1471
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: 500 Kb Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
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TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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    WESULF 5
US-08-427-640-1
; Sequence 1, Application US/08427640
; Patent No. 5658788
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SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
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LIBRARY: Pre-ma
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ORIGINAL SOURCE:
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TGGATCAACGACCGGAT 871
                                                          GACGGCTGCGGGCGCTCCACAAGCCGGGGGGTCTACACCCGCGTGGCCAACTATGTGGAC
                                                                                                                         GGGCCCCTGGCCTGCGAGAAGAACGGCGTGGCTTACCTCTACGGCATCATCAGCTGGGGT
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Pred. No. 1e-18;
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APPLICATION NUMBER: 07/689,4
FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.5%;
Best Local Similarity 50.8%;
Matches 342; Conservative
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MOLECULE TYPE:
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CITY: Indianapolis
STATE: IN.
COUNTRY: U.S.A.
ZIP: 46285
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ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
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STRANDEDNESS: Double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
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CCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGG
                                                                   TTCAGAAACCTGG.
                                                                                                                        GCAACTCCCGCCAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATC
                                                                                                                                                                                         CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT
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                                 CTCGGAGCGGCGGGCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGCC
                                                                                                   GCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGACA
                                                                                                                                                                     CTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.5
Best Local Similarity 50.8
Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/689
FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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Title OF INVENTION: CC
NUMBER OF SEQUENCES: 2
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                                                         ATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCCT 132
                                                                                                                               ACAATGAAAGAGATGAGATTCCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG
                                                                                                                                                                                                         AGAAAGAAGTTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCACT 1201
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                                     CGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTGCCGCACTGTGTGCCTTCCCCCGGCGGACC
                                                                                                                                                                                                                                                           GCTTCCAGGAGAGGTTTCCGCCCCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGG 511
                                                                                                           TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATT 625
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Lilly Corporate Center
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Pred. No. 1.6e-12;
0; Mismatches 286;
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US-08-427-640-3
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                                                                                                Matches 342;
                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/689,410
FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 3:
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TITLE OF INVENTION: COI
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
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                             SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pair
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50
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 GCACCGA-----CATAAAAAACCAGACATCTAAAAGGTGGTGCTAGGGGGACCAGGACCTGA 1141
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Pred. No. 1.6e-12;
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                                                                                 ; NAME/KEY: CDS
; LOCATION: (1)...(1137)
US-09-553-498-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09553498 Patent No. 6309861
                                                                                                                                                                                                                                   SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ambrosius, Dorothee
APPLICANT: Rudolph, Rainer
APPLICANT: Schaefiner, Joerg
APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: Process for the production of naturally folded and secreted
FILE REFERENCE: Case 20379
FILE REFERENCE: Case 20379
Query Match
Best Local Similarity
Matches 342; Conserv
                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: U5/09/553,498
CURRENT ETLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: EP99107412.1
PRIOR FILING DATE: 1999-04-26
                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                   ORGANISM: E. coli
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                                                                                                                                                   FEATURE:
                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1370 CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT 1429
                                                                                                                                                                                                               LENGTH: 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 TGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAAT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        689 TGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGT 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           749 CTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCT 808
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4.5%;
milarity 50.8%;
Conservative
  Score 75.4; DB 4; Length 1137; Pred. No. 1.7e-12; 0; Mismatches 286; Indels 45
           45;
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                    SEQ ID NO 9
LENGTH: 1137
TYPE: DNA
                                                                                                                                                 APPLICANT: Ambrosius, Dorthee
APPLICANT: Rudolph, Rainer
APPLICANT: Schaeffner, Joerg
APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED.
TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
TITLE OF INVENTION: CHAPERONES
FILE REFERENCE: 20381
FILE REFERENCE: 20381
                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09618869 Patent No. 6455279
                                                                      CURRENT APPLICATION NUMBER: US/09/618,869
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
ORGANISM: Escherichia coli
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                                                                                                                                                                                                                 Sequence 48, Application US/08811949
Patent No. 5840533
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Best Local :
                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (1)
           APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN.
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND,
                                                                                                                                           APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSH
APPLICANT: SASAKI, HIT
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Local Similarity 50.8%;
res 342; Conservative
ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                  GCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAGGTTACCAACTACCTAGACTGGA
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                                                                                                                                                             SAITO, YOSHIMASA
                                                                                                                                           SASAKI, HITOSHI
             OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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Pred. No. 1.7e-12;
0; Mismatches 286;
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INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
1314 base bairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/811
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-713-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  1112 CTCGGAGCGGCGGGCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGCC 117
                                        1490 TTCAGAAACCTGG-----
                                                                                                                                                                                                                                                                             1322 TTCCCT-----CTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAA 1369
                                                                                                                                                                                                                                                                                                                                             1262 ATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCCT 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1142 AGAAAGAAGTATTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCACT 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                           992 CTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCT 1051
                                                                                                                                                                                                                                       932 TGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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Local Similarity 50.8%;
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                                                                                                     GCAACTCCCGCCAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATC 1489
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                                                                                                                                                                                                                                                                                                                                                                                                  TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCTGCAGCTGAAATCGGATT 871
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                                                                              GCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGACA 1111
                                                                                                                                                                                                                                                                                                                      CGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCCTTCCCCCGGCGGACC 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAAT
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                       -----GCAAGACACCTGCCAGGGTGACTCTGGAGGCC 1534
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Pred. No. 1.8e-12;
0; Mismatches 286;
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US-08-883-795A-39
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Best Local Similarity
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APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-UN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Gravelle, Micheline
REGISTRATION UNUBER: 40,26
REFERENCE/DOCKET NUMBER: 7
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ORIGINAL SOURCE:
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ADDRESSEE: BERESKIN
                                                                           1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (416) 364-7311
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1223 TGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAAT 1282
                                                                                                                                                                                                                                                                                              1103 AGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACT 1162
                                                                                                                                                                                                                                                                                                                                                                  1028 AGGCCACTTCTGTGGTGGGGCGCTGATCCACCCCTGCTGGGTGCTCACTGCTGCCCACT 1087
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STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                               AGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCACT
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                                                                                                                                                   GCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGG 1222
                                                                                                                                                                                                                      GCACCGA-----CATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTGA 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 75.4; DB 2;
Pred. No. 2.2e-12;
0; Mismatches 286;
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                                                                               1201
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APPLICATION NUMBER: US/07/78
FILING DATE: 01-CCT-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 656,770
FILING DATE: 01-CCT-1984
SEQ ID NO:1:
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5344773-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATCHIT NO. 5344773

PATCHIT NO. 5344773

APPLICANT: WEI, CHA-MER; HSIUNG, NANCY; REDDY, VERMURI
LEMONTT, JEFFREY F.; DACKOWSKI, WILLIAM; DOUGLAS, RICHARD;
COLE, EDWARD S.; PUBCELL JR., RICHARD D.; LAU, DAVID TAI-YU
TITLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINOGEN
ACTIVATOR PRODUCED BY RECOMBIANT DNA
                                                                                                                                                                                                                                                                                                                      5344773-1
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 342; Conserv
1202 ACAATGAAAGAGATTGAGATTCCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261
                                            1146
                                                                                                                        1088 GCACCGA-----CATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTGA 1141
                                                                                                                                                                                           1028 AGGGCCACTTCTGTGGTGGGGGGCGCTGATCCACCCCTGCTGGTGGTGCTCACTGCTGCCCACT 1087
                                                                                                                                                                       1026 AGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCCACT 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
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                                                                                                    GCTTCCAGGAGAGGTTTCCGCCCCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGG
                                   TGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAAT
                                                                  AGAAAGAAGTTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCACT 1201
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                                                                                                                                                                                                                                              4.5%;
milarity 50.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    US/07/782,686
                                                                                                                                                                                                                                            Score 75.4; DB 6;
Pred. No. 2.5e-12;
0; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAVID TAI-YUI
                                                                                                                                                                                                                                              286;
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                                                                                                                                                                                                                                                                             Length 2457;
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RESULT 13
US-08-286-740-1
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                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
INFORMATION FOR SEQ ID NO:
                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEEAX: 415/952-9881
TELEEX: 910/371-7168
                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 05-AUG-CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                             NAME: Lee, Wendy M. REGISTRATION NUMBER:
                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San Francisco
STATE: California
COUNTRY: USA
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METHOD FOR SELECTING HIGH-EXPRESSING
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-286-740-1
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PCT-US95-09576-1
Sequence 1, Application PC/TUS9509576
GENERAL INFORMATION:
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Best Local Similarity 50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1028 AGGGCCACTTCTGTGGGGGGGGGCGCTGATCCACCCCTGCTGGGTGCTCACTGCTGCCCACT 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 7360 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1142 AGAAAGAAGAATTTCATGAGCAGAGATTTAGGGTGGAGAAGATATTCAAGTACAGCCACT 1201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1202 ACAATGAAAGAGATGAGATTCCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261
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                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                            TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING TITLE OF INVENTION: HOST CELLS
                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2868 CGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACC
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATT 2867
                                                                                                                                                                                                                                                                                                                                                                               AGTGTGGGAAGAGG-----CCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGGA 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCCT------CTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAA 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAAT
                                                                                                                                                                                                                                                                                  TTCGTGACAACAT 3300
                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGGTGTGTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCTGGGGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCGGAGCGGCCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCAGAAACCTGG-------GCAAGACACCTGCCAGGGTGACTCTGGAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGT 2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCCT 1321
                                                                                                                                                                                                                                                                                                                      TCAAAGCCACCAT 1661
                                                                                                                                                                                                                                                                                                                                                        GCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAGGTTACCAACTACCTAGACTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGACA 3107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                   GENENTECH, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75.4; DB 1;
Pred. No. 4.4e-12;
0; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
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PCT-US95-09576-1
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/28/
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDLUM TYPE: 5.25 inch, 360 Kb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 7360 bases
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                2988
                                                                                                                                                                                                                                                                                                                                                                                  1370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1028 AGGGCCACTTCTGTGGTGGGGGGCGCTGATCCACCCCTGCTGGTGGTGCTCACTGCTGCCCACT 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2634 ACCCCTTCCTGTGCGGGGCATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1202 ACAATGAAAGAGATGAGATTCCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2694 GCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGG
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ZIP: 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.5%;
Local Similarity 50.8%;
hes 342; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCCTTGCCTGATGGGTCCT 1321
CCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCTGGGGCCTGG
                                                                                                                                                              TTCAGAAACCTGG-------GCAAGACACCTGCCAGGGTGACTCTGGAGGCC
                                                                                                                                                                                                                                                 GCAACTCCCGCCAACTCTATGACCACATGATTGATGATGATGATCTGTGCAGGAAATC 1489
                                                                                                                                                                                                                                                                                                                                                                             CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCCCT------CTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAA 1369
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                                                  CCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGG
                                                                                                         CTCGGAGCGGCCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGCC
                                                                                                                                                                                                                                                                                                                             CTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCAGCTGCCGGACTGGAGCGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCACT 1201
                                                                                                                                                                                                                   GCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGACA
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Pred. No. 4.4e-12;
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RESULT 15
US-08-148-910-2
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                                                                                                                                                                                                         Query Match
4.4%; Score 73.8; DB 1; Length 329;
Best Local Similarity 59.6%; Pred. No. 2.6e-12;
Matches 164; Conservative 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/OCCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: doul TOPOLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE: CONA ORIGINAL SOURCE: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 500 Kb Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1441 CAACTETATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT 1500
                                                                                                                                                        1381 TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC 1440
                                                                                                                                                                                                                                                                                                                         ORGANISM: huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Takeshi SHIMOMURA et al.
TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding Said Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3288 TTCGTGACAACAT 3300
                1501 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCCTGACCTGTGAGAAGGACGGCACC 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                         112 GÁGGTCTACGGCGCCGACATCAGCCCCAACATGCTCTGTGCCGGCTACTT----CGACTGC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/148,910 FILING DATE: No. 5466593ember 5, 1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 805 Fift
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 20005
                                                                                                                                 52 TCCAGCTCCCTGCGGGAGGCCCTGGTCCCCCTGGTCGCCGACCACAGTGCAGCAGCCCT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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805 Fifteenth Street, N.W., #700
202-371-8856
                                                                                                                                                                                                                                                                                                        Quick-cloneTM human liver cDNA (Clonetech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                         double
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Search completed: March 6, 2003, 19:40:07 Job time: 91.5 secs

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Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-912-559-1
1683
1 atgtttgccaggatgtctga.....aaagtgaaagtggcttctaa 1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6, 2003, 18:44:22;
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   10 US-09-912-559-1
10 US-09-880-107-1668
10 US-09-884-761-11164
10 US-09-880-107-1612
11 US-09-880-107-1612
11 US-09-880-107-1612
11 US-09-880-107-1612
11 US-09-864-761-27791
11 US-09-969-271-6
12 US-09-969-271-6
13 US-09-974-298-144
14 US-09-879-792-3
15 US-09-879-792-3
16 US-09-879-792-11
17 US-09-879-792-11
18 US-09-879-792-16
18 US-09-978-295A-68
18 US-09-978-295A-68
18 US-09-978-295A-68
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18 US-09-978-12A-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search time 127.5 Seconds (without alignments) 8816.543 Million cell updates/sec
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 552, App
Sequence 552, App
Sequence 27791, A
Sequence 27791, A
Sequence 5, Appli
Sequence 144, App
Sequence 144, App
Sequence 14, Appl
Sequence 11, Appl
Sequence 68, Appl
                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09912559

Patent No. US20070142316A1

GENERAL INFORMATION:
APPLICANT: ROEMISCH, JUERGEN
APPLICANT: STOCHER, HANS-ARNOLD
APPLICANT: STOCHER, HANS-TOLD
APPLICANT: LANG, WIEGAND
APPLICANT: LANG, WIEGAND
APPLICANT: WELNER, THOMAS
APPLICANT: WELNER, THOMAS
APPLICANT: NERLICH, CLAUDIA
APPLICANT: NERLICH, CLAUDIA
APPLICANT: MUTH-NAUMANN, GUDRUN
TITLE OF INVENTION: MUTHANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
TITLE OF INVENTION: DETECTION METHODS USING SPECIFIC ANTIBODIES
FILE REFERENCE: 06478.1457
CURRENT APPLICATION NUMBER: US/09/912,559
CURRENT FILING DATE: 2001-07-26
CURRENT FILING DATE: 2001-07-26
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; ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: DE 100 50 040.4
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: DE 100 52 319.6
PRIOR FILING DATE: 2000-10-21
PRIOR APPLICATION NUMBER: DE 101 18 706.8
PRIOR APPLICATION NUMBER: DE 101 18 706.8
PRIOR APPLICATION NUMBER: DE 101 18 706.8
PRIOR PILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity 100.0%;
Matches 1683; Conservative 0
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US-10-176-985-63
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APPLICANT: HOTNE, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF 520 ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 1668
LENGTH: 3008
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D49742
US-09-880-107-1668
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                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: STORMISCH, JUERGEN
APPLICANT: STORMISCH, HANS-ARNOLD
APPLICANT: STORMISCH, CHANS-ARNOLD
APPLICANT: LANG, WIEGAND
APPLICANT: LANG, WIEGAND
APPLICANT: LANG, WIEGAND
APPLICANT: WEIMER, THOMAS
APPLICANT: NUTH-NAUMANN, GUDRUN
TITLE OF INVENTION: MOTANN'S OF THE FACTOR VII-ACTIVATING PROTEASE AND
TITLE OF INVENTION: MOTANN'S OF THE FACTOR VII-ACTIVATING PROTEASE
FILE REFERENCE: 06478.1457
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: DE 100 36 641.4
PRIOR FILING DATE: 2000-07-26
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEG ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 12
LENGTH: 1683
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FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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                                                                                                                                                                                                                                                   Sequence 11164, Application US/09864761 Patent No. US20020048763Al GENERAL INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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FEATURE:
OTHER INFORMATION: MAP TO AC006097.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
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Sequence 552, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Seets
TITLE OF INVENTION: Seets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT APPLICATION NUMBER: US/09/33,617
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SEQ ID NO 11164
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Best Local Similarity
                                                                                                                                                                                       -09-954-456-552
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
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FILING DATE: 2001-01-50
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE:
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NUMBER: US 09/774,203
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NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 552
LENGTH: 2036
TYPE: DNA
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Best Local Similarity 49.8%;
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OR FILING DATE: 2000-09-26
OR APPLICATION NUMBER: US/60/235,638
OR FILING DATE: 2000-09-26
OR APPLICATION NUMBER: US/60/235,711
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: US/60/235,720
OR FILING DATE: 2000-09-27
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APPLICATION NUMBER: US/6
FILING DATE: 2000-09-20
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APPLICATION NUMBER: US/50/234,923
FILING DATE: 2000-09-25
APPLICATION NUMBER: US/50/235,134
FILING DATE: 2000-09-25
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  TGGGTGCTCACTGCCCACCTGCACCGACATAAAAACCCAGACATCTAA----
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                                                           --GCTGGCCGCCATCTACATCGGGGACAGCTTCTGCGCCGGGAGCCTGGTCCACACCTGC
                                                                                             CCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGGGCGCTGATCCACCCCTGC
                                                                                                                                  CTGCGGCCACGTATCATCGGCGGCTCCTCCTCGCTGCCCGGCTCGCACCCCTG------
                                                                                                                                                        GGAGGCTTTAAGAGCACGGCGGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCTCGCTG
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Pred. No. 8.2e-26;
0; Mismatches 559;
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Length

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Gaps

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1323 1065 1265 1005 1212 1044 765

825

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864 585 804 528

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APPLICANT: Scherf Uwe
APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 4421-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION UMBER: US 60/237,054
PRIOR APPLICATION UMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1612
LENGTH: 2036
TYPE: DNA
CORNAITSM: Homo sabiens
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US-09-880-107-1612
Sequence 1612, Application US/09880107
Patent No. US20020142981A1
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                             Query Match
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                                                                                   OTHER INFORMATION: Genbank Accession No. US20020142981A1 D14012
                                                                                                    FEATURE:
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y Match 7.0%;
Local Similarity 49.8%;
hes 607; Conservative
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Score 117.6; DB 10
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AACATGCTCTGTGCCGGCTACTT----CGACTGCAAGTCCGACGCCTGCCAGGGGGGACTCA 1797
                                      AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCT 1527
                                                                                                                    TGGGGCCACTTGGATGAGAACGTGAGCGGCTACTCCAGCTCCCTGCGGGAGGCCCTGGTC
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PRIOR FILLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILLING DATE: 2001-01-30
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                                                                                                                  NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine
SEQ ID NO 27791
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: MAP TO AC006097.1
OTHER INFORMATION: EXPRESSED IN PLACENTA,
OTHER INFORMATION: EXPRESSED IN LUNG, SIG
                                                              ORGANISM: Homo sapiens
                                                                                 TYPE: DNA
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 2000-0
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
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US-09-864-761-27791
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US-09-969-271-6
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Sequence 6, Application US/09969271

Patent No. US20020098179A1

GENERAL INFORMATION:
APPLICANT: Pfizer Inc. (All designated States except GB APPLICANT: Pfizer Limited (GB and EP (GB) only)
TITLE OF INVENTION: Pharmaceutical Combinations
FILE REFERENCE: PCS10951APME
CURRENT APPLICATION NUMBER: US/09/969,271
CURRENT APPLICATION NUMBER: US/09/969,271
PRIOR APPLICATION NUMBER: GB 0025473.0
PRIOR APPLICATION NUMBER: GB 0025473.0
PRIOR FILING DATE: 2000-10-17
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CAGGAAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAAGTCAAGCTGATTGCCCAACACTTTGT
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                                                                               TGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGT
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EXPRESSED IN BRAIN, SIGNAL = 1.1
EXPRESSED IN BORE WARROW, SIGNAL = 1
EXPRESSED IN BOLE WARROW, SIGNAL = 1
EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
WT HIT: S83182.1, EVALUE 8.00e-60
SWISSPROT HIT: 025464, EVALUE 1.00e-03
EST_HUMAN HIT: T68666.1, EVALUE 7.00e-55
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s; Pred. No. 2.1e-26;
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Pred. No. 9.1e-13;
0; Mismatches 286;
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SEQ ID NO 5
LENGTH: 2519
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local :
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APPLICANT: Pfizer Limited (GB and EP (GB) only)
TITLE OF INVENTION: Pharmaceutical Combinations
FILE REFERENCE: PCS10951APME
CURRENT APPLICATION NUMBER: US/09/969,271
COURSENT FILING DATE: 2001-10-01
PRIOR APPLICATION UNUMBER: US/09/969,273
ORDERING PRIOR DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
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                                                                                                           CGTCCCGCTGTGCCCAGGAGCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACC
                                                                                                                                          ATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCCT 1321
                                                                                                                                                                               TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATT 1322
                                                                                                                                                                                                                    ACAATGAAAGAGATGAGATTCCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261
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                                                                        -CTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAA 1369
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Pred. No. 1.2e-12;
0; Mismatches 286;
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US-09-974-298-144
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Best Local S
Matches 342
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SEQ ID NO 144
LENGTH: 2641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-55-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure LOCATION: 2635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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  1443 CGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACC 1502
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 50.8 es 342; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGG 1594
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                                   ATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCCT 1321
                                                                                               ACAATGAAAGAGATGAGATTCCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261
                                                                                                                                                                                       AGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCACT 1201
                                                                                                                                                                                                                                 GCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGG 1328
                                                                                                                                                                                                                                                                      GCACCGA-----CATAAAAACCAGACATCTAAAAGGTGGTGCTAGGGGGACCAGGACCTGA 1141
                                                                           TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATT 1442
                                                                                                                                                      \tt TGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAAT
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50.8%;
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Pred. No. 1.2e-12;
0; Mismatches 286;
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SEQ ID NO 33
LENGTH: 614
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Best Local Similarity
Matches 175; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xiao, Yonghong
APPLICANT: Gedrich, Richard
TITLE OF INVENTION: Regulation of Human Transmembrane Serine
TITLE OF INVENTION: Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/283,353
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/283,648
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 02973.00035
CURRENT APPLICATION NUMBER: US/09/879,792
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/211,224
PRIOR FILING DATE: 2000-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                         1501
                                                                                             1441 CAACTCTATGACCACATGATTGATGACACATATGATCTGTGCAGGAAATCTTCAGAAACCT 1500
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                                 GGGCAAGACCACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC
                                                                         TTGGTCTATGACAGCTACCTTACCCCAAGGATGATGTGTGCCGGGGGATCTACGAGGA---
                                                                                                                                                    TCTCCCTTCCTCCGAGAGGTTCAGGTCAACCTCATTGACTTCAAGAAGTGCAATGACTAC
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GGGAGGGACTCCTGCCAGGGAGACAGTGGAGGACCTCTCTGTGAGCAGAACAATCGC
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Conservative
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                                                                                                                                                                                                                               Score 72.8; DB 10;
Pred. No. 3.1e-12;
0; Mismatches 122;
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US-09-888-615-45
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Best Local Similarity 56.2%;
Matches 172; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
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                                 1675 GGCTTC 1680
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CGATTC
                                                                     GTGTACACCAAAGTGACAGAAGTTCTTCCCTGGATTTACAGCAAGATGGAGAGCGAGGTG
                                                                                                      GTCTACACCCAAGTTACCAAATTCCTGAATTGGATCAAAAGCCACCATCAAAAGTGAAAGT 1674
                                                                                                                                        GGCAGAGACTCCTGCCAGGGAGACAGCGGGGGGGCCTCTTGTCTGTGAGCAGCAACAACCGC 1476
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CHARYDCZAK, GLEN
MANNING, GERARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB 10;
Pred. No. 1.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1614;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT 13 US-09-879-792-11

Sequence 11, Application US/09879792 Patent No. US20020061850A1 GENERAL INFORMATION:

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                                        CURRENT APPLICATION NUMBER: US/09/879,792
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/211,224
PRIOR FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 60/283,353
PRIOR APPLICATION NUMBER: US 60/283,648
PRIOR APPLICATION NUMBER: US 60/283,648
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Patent No. US20020061850A1
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Best Local :
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                                                                                                                                                                                                                                                      APPLICANT: Xiao, Yonghong
APPLICANT: Gedrich, Richard
TITLE OF INVENTION: Regulation of Human Transmembrane Serine
TITLE OF INVENTION: Protease
FILE REFERENCE: 02973.00035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/211,224
PRIOR FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 60/283,353
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/283,648
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
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CURRENT FILING DATE: 2001-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-06-12 NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xiao, Yonghong APPLICANT: Gedrich, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT
  NUMBER OF
                           PRIOR FILING DATE: 2001-06-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1445 TTGGTCTATGACAGTTACCCTTACCCCAAGGATGATGTGTGCTGGGGGACCTTCGT---GGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1385 TCCCCCTTCCTCCGGGAGGTGCAGGTCAATCTCATCGACTTCAAGAAATGCAATGACTAC 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1381 TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1441 CAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT 1500
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Local Similarity 56.2%;
nes 172; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTACACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGT 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCAGAGACTCCTGCCAGGGAGACAGCGGGGGGGCCTCTTGTCTGTGAGCAGAACAACCGC
SEQ ID NOS: 36
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Pred. No. 1.8e-10;
0; Mismatches 125
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                                             (Docket
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                                               US20020061850A1 LIO-81-WO)
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; FEATURE:
; NAME/KEV: misc_feature
; LOCATION: (1)...(1230)
; OTHER INFORMATION: n = 1
US-09-879-792-35
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APPLICANT:
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Best Local Similarity
                                                                                                        APPLICANT:
                                                                                                                                                              APPLICANT:
CURRENT APPLICATION NUMBER: US/09/978,295A CURRENT FILING DATE: 2001-10-15
                                  APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGA 1549
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                                                                                         Williams, P. Mic
Wood, William I
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                                                                                                                                         Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                           Grimaldi,
                                                                                                                                                                                                                                                                                                                                         Godowski, Paul
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Desnoyers, Luc
                                                                                                                           Tumas, Daniel
                                                                                                                                                                                                   Paoni,
                                                                                                                                                                                                                                                   Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                      Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                      Gurney, Austin L
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                                                                                                                                                                                                                                  Napier, Mary A.
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                                                                                                          Mickey
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Pred. No. 4.6e-10;
0; Mismatches 121;
                                                                       Polypeptides
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PPLICATIO	ILING DAT	PPLICATIO	PPLICATI	ILING DAT	PPLICATIO	ILING DAT	ILING	PPLICATIO	ILING DAT	ILING	PPLICATIO	ILING DAT	TLING DAT	PPLICATIO	ILING DAT	APPLICATION	PPLICATIO	LING	PPLICATIO	ILING DAT	ILING DA	PPLICATION	TLING DATE	TLING DATE	PPLICATION	TLING DATE	TLING DATE	PPLICATION	PLICATION LING DATE	ILING DATE	PPLICATION	PPLICATION	PPLICATION	LING DATE	ILING DATE	PPLICATION	TLING DATE	ILING DATE		PPLICATION	LING DATE	PPLICATION	PPLICATION	TLING DATE	Z FI	PPLICATION	TLING DATE	TLING DATE	PPLICATION	PPLICATION	ILING DATE	ATT.
NUMBER: 60	998-05-07	MBER: 60	NUMBER:	1998-05-07	NUMBER: 60	1998-05-07	98-05-07	NUMBER: 60		98-05-07	NUMBER: 60	98-05-06	TY98-05-06	NUMBER: 6	1998-05-05	ER: 60	NUMBER: 6	1998-04-29	NUMBER: 60	-04 -	98-04-29	NUMBER: 60	-04-	98-04-29	NUMBER: 60	1998-04-	98-04-29	NUMBER: 60	-04 -	1998-04-29	98-04-2 BER: 60	NUMBER: 60	NUMBER: 6	98-04-23	98-04-	NUMBER: 60	-04-	98-04-22	MBER: 60	1999-04-	98-04-21	90-04-2 BER: 60	NUMBER: 60	-04-15	998-04-15	NUMBER: 60	NUMBER: 60/081819 : 1998-04-15	998-04-15	MBER: 60	NUMBER: 60	998-04-09	ER: 60

PRIOR

OR APPLICATION NUMBER: 09/918585
OR FILING DATE: 2001-07-30
OR APPLICATION NUMBER: 60/062250
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Search completed: March 6, Job time : 139.5 secs

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## SUMMARIES

AUTHORS	SOURCE ORGANISM	AX383955 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	RESULT 1	45	4.3	41 42	4 W 20 20 20	38	30	ωω 54	ωι	2 31 2 1	30	28	26 27	25	23	21	19 20							ာ ထ ၁	<b>-</b>			1 2 1	Result No.
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RESULT \$83182 LOCUS DEFINITION

VERSION KEYWORDS SOURCE REFERENCE ACCESSION ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2408) Choi-Miura, N.H., Tobe, T., Sumiya, J., Nakano, Y., Sano, Y., Mazda, T. and Tomita, M. Homo \$83182 \$83182 hyaluronan-binding protein=hepatocyte homolog [human, plasma, mRNA, 2408 nt] Homo sapiens homolog sapiens plasma [human, plasma, GI:1836158 2408 bp mRNA growth factor activator PRI 11-FEB-1997

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J. Biochem. 119 (6), 1157-1165 (1996)
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GWGVPETGKGSRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNIQKFPGQDTCQGD
SGGPLTCEKDGTYYVYGIVSWGLECGKRPGVYTQVTKFLNWIKATIKSESGF"
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/note="hepatocyte growth factor activator homolog; Method:
conceptual translation with partial peptide sequencing;
This sequence comes from Fig. 3B; PHBP"
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1597 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC  1561 TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAGAAGAGGGCCAGGGGTCTAC	517	Db
501	421 CCTTACACAGGTCCCAGCTGCTGCTGCAGGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 480	Qy
1441 CAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT 	361 457	Оу
1381 TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC	9Y 301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAAGTGCAAAATACGTGCAAGGACAACCCATGT 360	Оy
	241 CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG 300	Оy
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1141 AAGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCAC 	9y 61 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120	ОУ
1081 1177	1 ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60	Оy
1021 ATGCCCCAGGGCCACTTCTGTGGTGGGGCGCTGATCCACCCCTGCTGGGTGCTCACTGCT	Query Match 99.8%; Score 1679.8; DB 6; Length 3008; Best Local Similarity 99.9%; Pred. No. 0; Matches 1681; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Q Be
961 ACGGCGGGCAAGCACCCATGGCAGGCGTCCCAGTCCTCGACTTGCCTTCGACCATCTCC	/db_xref="taxon:9606" Qy /note="EMBL/GenBank Accession No. D49742" Qy BASE COUNT 791 a 837 c 703 g 677 t Db	BASI
901 TGTGGAAAGACTGAGATAGCAGAGAGAGGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGC	EATURES LOCATION/Qualifiers  Source 1. 3008  /organism="Homo sapiens"	FEAJ
* 841 GTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAAGCAAG	THORS Alvares, C., Horne, D., Peres-da-Silva, S. TLE Gene expression profiles in liver cance Gene expression profiles in liver	AU TI
781 GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGAC 	SOURCE human:  ORGANISM Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	sou
721 GGGGAACACAATTTCTGCAGAAACGCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAA 	I'LIN Sequence 1668 from Patent W00229103. ION AX409021 N AX409021.1 GI:21441726 DS .	ACC VER
/ 661 CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT	AX409021 3	RES AX4
7 601 TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC	yy 1681 TAA 1683 Qy b 1777 TAA 1779 Db	рь
7 541 CAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC		Оу
481 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC	1561 1657	Оy

Ouery Match  99.8%: Score 1679.8; DB 9; Length 3008;  Best Local Similarity 99.9%; Pred. No. 0;  Matches 1681; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  1 ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAGACA 60	/codon_start=1 /prodein_id="BaA08576.1" /protein_id="BaA08576.1" /protein_id="BaA08576.1" /protein_id="BaA08576.1" /db_xref="GI:1345398" /translation="MFARMSDLHVLLMALVGKTACGFSLMSLLESLDPDWTPDQYDY /translation="MFARMSDLHVLLTQSEPYTRCVCKHPYTGPSCSQVPVPVCRPNPCQ RSTCSRHKRSKFCTACEPDDFKGKFCTGTGPSCSGVVPVCRPNPCQ RGATCSRHKRSKFCTACEPDDFKGKFCELEGDDCYVGDGYSYRGKMRTVNGHACLYW NSHLLLOENYNMFWEDAETHGIGEHNFCCRNPDADERPWGTIKVTNUKVKMEYCDVSAC SAQDVAY DEESPTEPSTHGTGENFCCRNPDADERPWGTIKVTNUKVKMEYCDVSAC SAQDVAY DEESPTEPSTHCTHGTGENFCTKTHUKVVLODQDLKKEEFHEQSFRV ERIFKYSHYNERDEIPHNDIALLKKFVDGHCALESKYVKTVCLDQDSFSGSECHIS GWGVTETGKGSRQLLDAKVKLIANTLCNSRQLYDMIDDSMICAGNIQKFGODTCOGD SGGPLTCEKDGTYXVYGIVSWGLECGKRPGVYTQVTKFLNWIKATIKSESGF"  polyA_site	0	HUMHGFAL JOOBS bp mRNA linear PRI 10-FEB-1999 LOCUS HUMAN MINA PRI 10-FEB-1999 DEFINITION HUMAN MRNA for HGF activator like protein, complete cds.  ACCESSION D49742.1 G1:736706 EXEWORDS HGF activator like protein; serin protease.  SOURCE HOMO sapiens cDNA to mRNA. ORGANISM Homo sapiens cDNA to mRNA. EUKALTYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 3008)  AUTHORS Kitamura, N.	1621 ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGACTTC 1680	
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AGACTGTGTGCTTGCCTGATGGGTCC 1320 AGAGAATCTATGGAGGCTTTAAGAGC 960 ATGTCTCAGCCTGCTCAGCCCAGGAC 840 ATGACTGCTATGTTGGCGATGGCTAC 600 CCAAGTTCACCTGTGCCTGTCCCGAC 540 CCAAGCTGATCCATGCCAGCCCAAC AGGTGGTGCTAGGGGACCAGGACCTG 1140 GGAGGATGCTGAAACCCATGGGATT 720 AGGTGGTGCTAGGGGACCAGGACCTG GAGAATCTATGGAGGCTTTAAGAGC 1056 GGAGGATGCTGAAACCCATGGGATT 1236 816 996 900

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                                 Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 50 Row: g Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 203021:
                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/cdna/contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Baylor College of Medicine Human
Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (06-JUN-2002) National Institutes of Gene Collection (MGC), Cancer Genomics Office, Institute, 31 Center Drive, Room 11A03, Bethesd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2251 bp mRNA linear PRI 27-, Homo sapiens, hyaluronan binding protein 2, clone MGC:34485 IMAGE:5187066, mRNA, complete cds. BC031412
                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
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[ bases 1 to 2251)
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                          Location/Qualifiers
/organism="Homo sapiens"
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Martin,
                                                                                                                                                                                                                                                                                                                         Office, National Cancer
Bethesda, MD 20892-2590
                                                                                         information can be found
                                                                                                                                 S.W., F. R.G.,
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National Cancer
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                                                         CACTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC
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SYEDYNQEENTSSTLTHAENPDWYYTEDQADPCQPNPCEHGGDCLWHGSTFTCSCLAP
FSGRKCQKYQMTCKNDNGGRGQCLITOSPPYYRCVKHPYTGPSGSQVVPVCRPNPCQ
NGATCSRHKRRSKFTCACPDQFKGKFCEIGSDCYVGDGYSYRGKMNRTWNQHACLYW
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SAQDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQAALQSS
LPLTISMPCCHFCGGALHIPCWVLTAAHCTDIKTRHLKVVLGDQDLKKEEFHERDSFRV
EKIFKYSHYMERDBEIPHNDIALKLKPVDGHCALESKYVKTVCLPDGSFPSGSECHIS
GWGVTETGKGSRQLLDAKVKLIANTLCNSRQLYDHNIDDSNICAGNLOKPGGODTCQGD
SGGPJTCEKGTYVVGGTVSWGLECGKARPGVYTQVTKFLNMIKATIKSESGF"

8 609 c 533 g 483 t
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/protein_id="AAH31412.1"
/db_xref="GI:21618649"
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/tissue_type="Colon, Kidney, Sto
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="LocusID:3026"
/db_xref="taxon:9606"
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                                                                                                                                                ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC 1680
                                                                                                                                                                                                                                                                                                        TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGGGAAGAGGCCCAGGGGTCTAC
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Conter and Conter
Conter and Conter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2119 | Mus musculus, clone MGC:28705 BC031775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution informati
through the I.M.A.G.E. Consortium/LINL at: http://in
Series: IRAK Plate: 37 Row: n Column: 14
This clone was selected for full length sequencing by
passed the following selection criteria: Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-JUN-2002) National Institutes of Health, Mammaliar Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
NIH-MGC Project URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 2119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      passed the following identity to protein
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Similarity 82.:
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1. .2119
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1180	1 TGCTAGGGGACCAGGACCTGAAGAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGCAGA	112
1120 1049	1 CCTGCTGGGTGCTCACTGCCCACTGCACCGACATAAAAACCAGACATCTAAAGGTGG 	, 106
1060	1 CGCTGCCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGCGCTGATCCACC	, 100
1000 929	1 TCTATGGAGGCTTTAAGAGCACGGCGGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCT	94
940 869	1 AGCTTCCGGGGTTTGACTCCTGTGGAAAGACTGAGATAGCAGAGAGAAGAAAAATCAAGAGAAAA	88
880	1. CAGCCTGCTCAGCCCAGGAGGTTGCCTACCCAGAGGGAAAGCCCCACTGAGCCATCAACCA	, 82 5 75
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700 629	1 CGTGCCTTTACTGGAACTCCCACCTCCTGCAGGAGAATTACAACATGTTTATGGAGG	) 64
640 569	31 GCTATGTTGGCGATGGCTACTCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATG 	y 58
580 509	21 TCACCTGTGCCTGTCCCGACCAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACT 	y 52
520 449	11 GCAGGCCAAACCCCTGCCAGAATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGT 	y 46 b 39
460 389	11 ACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTCCCCAAGTGGTTCCTGTAT	y 40 b 33
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                                                               Direct Submission

Direct Submission

Direct Submission

Submitted (29-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 31, 2001 this sequence version replaced gi:14596344.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw., SWISSPROT; TT; TREMBL; Wp:, WORMPEP; Information on the WORMPEP hits sequence was generated from part of hacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/REP/Chilo

REDIFORM SEQUENCE OF THE SEQUEN
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vector sequences.

* NOTE: This is a 'working draft' sequence. It currently

* CORSISTS of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 157750: contig of 157750 bp in length.
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HTG; HTGS_PHASE2; HTGS_CANCELLED.
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                                                                                                                                                                                                          Submitted (04-DEC-1998) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing Technology. Data may contain low quality seq uence and BAC/Cosmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Sequence from overlapping clone RP11-481H12
(AL133482). Assembly confirmed by restriction diges
4 42671 c 41477 g 51788 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11.1"
22142. .22187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="10"
/clone="RP11-190F19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of clone RP11-481H12 is at 111825 in this sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 261.2; DB 9; Pred. No. 5.1e-67; 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 188349;
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Matches 270; Conserv
                                                                                                                                                                                                                                  Best Local Similarity 84. Matches 271; Conservative
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             GGGAACCTTCAGAAGCCCGGATCAGACACCTGCCAGGGTGACTCGGGGGGGCCCTCTAACC 192
                                                 GGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACC
                                                                                                                                                             ACAGAAACAGGGGAAGGGTCCCGCCAGCTCCTGGATGCTAAAGTCAAGCTAATCGCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGTCCCTCCAGTCCTCGCTGCCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGT 57446
                                                                                                                                                                                                                                                                                                                                                                                                School Juridical Person Nihon University (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for examining ischemic conditions Patent: WO 0188188-A 123 22-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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/db_xref="taxon:9606"
/chromosome="10"
/map="10925"
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105 c 111 g
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Pred. No. 4.6e-66;
0; Mismatches 20
                                                                                                                                                                                                                                                    Score 241; DB 6
Pred. No. 3e-61;
                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                   TGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAG 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGAGAAGGATGGAACTTACTACGTCTACGGGATTGTAAGCTGGGGCCAGGAATGTGGG
                                                  Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C. Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (bases 1 to 200960)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Alla, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarrata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzeerald, M., FitzHugh, W., Gage, D., Fand, Plerren, M., Hagos, B., Horton, L., Graham, L., Graham, T., Graham, T.,
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Collongelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Collongelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Collongelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Collongelo, M., Collins, S., Collongelo, M., Chazaro, M., Chazaro, Choepel, Y., Collongelo, M., Chazaro, M., Chazaro, M., Chazaro, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K.,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-116D4
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Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.
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Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 26, 2002 this sequence version replaced gi:21538062.
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                       100157 100256: gap of 100 bp
100257 117204: contig of 16948 bp in length
117205 117304: gap of 100 bp
117305 135487: contig of 18183 bp in length
135488 135587: gap of 100 bp
135588 160179: contig of 24592 bp in length
160180 160279: gap of 100 bp
160280 190016: contig of 29737 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consists of 16 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

19807: contig of 19807 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence.
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Assembly program: Phrap; version 0.960731
Consensus quality: 196003 bases at least 040
Consensus quality: 198358 bases at least 030
Consensus quality: 19836 bases at least 030
Consensus quality: 19896 bases at least 020
Insert size: 210000; agarose-fp
Insert size: 199460; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 9.0 in Q20 bases; agarose-fp Quality coverage: 9.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19908 20732: contig of 825
20733 20832: gap of 20833 21673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L23373
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36072
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31955 32054:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25273 25372: gap of 100 bp
25373 28544: contig of 3172 l
28545 28644: gap of 100 bp
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21771 232
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                                                                                                                                                                                                                                                                                                                                                                                                                          46254:
                                                                                                                                                                                                                            6254: gap of 100 bp
58025: contig of 11771 bp in length
8125: gap of 100 bp
100156: contig of 42031 bp in length
00256: gap of 100 bp
117204: contig of 16948 bp in length

    Genome Center

                                                                                                                                                                                                                                                                                                                                                                                                       171: gap of 100 bp 46154: contig of 9983 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              770: gap of 100 bp
23296: contig of 1526 bp in length
396: gap of 100 bp
25272: contig of 1876 bp in length
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21670: contig of 838 bp in length
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gap of 100 pp
30: contig of 10844 bp in length
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Miyazawa, K.,

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                                                                                                                                                                                                                                                                               958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                               GCTGCCCACTGCACCGA 1094
                                                                                                                                                                                                                                         AGCACAGCAGGCAAGCACCCGTGGCAGGTGTCCCTGCAGACCTCACTGCCGTTGACCACC 64429
                                                                                                                                                                                                                                                               AGCACGGCGGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCTCGCTGCCTCTGACCATC 1017
                                                                                                                                                                   TCCATGCCCCAAGGCCACTTCTGTGGGGGGCGCCCTGATCCACCCCTGCTGGGGTGCTCACT 64489
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32055, .36071
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25373. .28544
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20833. .21670
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/db_xref="taxon:10090"
/clone="RP23-116D4"
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/note="assembly_fragment"
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117305. .135487
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100257. .117204
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36172. .46154
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Pred. No. 1.3e-38;
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Best Local Similarity 50.9%;
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                                                                                         646 CTTTACTGGAACTCCCACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCT
                                                                                                                               857
                                                                                                                                                                   586
                                                                                                                                                                                                       797
                                                                                                                                                                                                                                                                               737
                                                                                                                                                                                                                                                                                                                   469 AACCCCTGCCAGAATGGGGCTACCTGCTCCCGGCATAAGCCGGAGATCCAAGTTCACCTGT
                 GAAACCCATGGGATTGGGGAACACAATTTCTGCAGAAACCCCAGATGCGGACGAAAAGCCC 765
                                                                                                                                                                                                                                                                               AGCCCATGTCTGAACGGAGGCACCTGCCACCTGATTGTGGGCACAGGGACCAGCGTCTGC
                                                       CTGGCCTGGAATTCTGACCTGCTCTACCAGGAGCTGCACGTGGACTCAGTGGCTGCT
                                                                                                                               CTGGGAAATGGTACAGAGTACCGAGGCGTGGCCAGCACCGCTGCCTCGGGCCTGAGCTGC
                                                                                                                                                                 GTTGGCGATGGCTACTCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGC
                                                                                                                                                                                                       ACCTGCCCGTTGGGCTATGCTGGGCGGTTCTGTAACATTGTTCCCACAGAGCACTGCTTC
                                                                                                                                                                                                                                         GCCTGTCCCGACCAGTTCAAGGGGAAATTCTGTGAAATAGGT---TCTGATGACTGCTAT 585
                                                                                                                                                                                                                                                                                                                                                     621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse hepatocyte growth factor activator gene: its only in the liver but also in the gastrointestinal Biochim. Biophys. Acta 1491 (1-3), 295-302 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-MAR-1999) Pathology, M: Kihara, Kiyotake, Miyazaki 889-1692,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2035)
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Direct Submission
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3 629 c 578 g 418 t
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PPRDSITVVLGQHFFNRTTDVTQTFGIEKYVPYTLYSVFNPNNHDLVLIRLKKKGERC
AVRSQFVQPICLPEAGSSFPTGHKCQIAGWGHWDENVSSYSNSLLEALVPLVADHKCS
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IVPTEHCFLGNGTEYRGVASTAASGLSCLAWNSDLLYQELHVDSVAAAVLLGLGPHAY
CRNPDKDERPWCYVVKDNALSWEYCRLTACESLARVHSQTPEILAALPESAPAVRPTC
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QPCRFPFRYGGRMLHSCTSEGSAYRKWCATTHNYDRDRAWGYCAEVTLPVEGPAILDP
CASGPCLNGGTCSSTHDHGSYHCSCPLAFTGKDCGTEKCFDETRYEYFEVGDHWARVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPEVYGADISPNMLCAGYFDCKSDACQGDSGGPLVCEKNGVAYLYGIISWGDGCGRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="hepatocyte growth factor activator"
/protein_id="AAF02489.1"
/db_xref="GI:6049172"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MGRQAWISSLCPLPRPCPFLLLLLLLLVVPRGAQPQAGRNHTEPP/
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                                                                                                                                                                                                                                                                                                                                                                       Score 129.8; DB 1
Pred. No. 1.8e-27;
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Mismatches
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2, Japan
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Indels Length

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RESULT 13
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van Adelsberg, J.S., Sehgal, S., Kukes, A., Brady, C., Bar Yang, J. and Huan, Y.
Direct Submission
Submitted (13-JAN-2000) Medicine and Anatomy and Cell Submitted (13-JAN-2000) Medicine to Submitted (13-JAN-2000) Medicine and Submitted (13-JAN-2000) Medicine and Anatomy and Cell Submitted (13-JAN-2000) Medicine and Cell Submitted (13-JAN-2000) Medici
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EGHVEQCGCMEGQARCEDTHHTACLSSFCLNGGTCHLJYGTGTSVCTCPLGYAGRECN
IVPTEHCFLGNGTEYRGVSTAASGLSCLAWNSDLLYGLHVDSVAAAVLLGGHAY
CRNDDXDERWCYVVKDNALSWEYCRLTACESLARVHSQFPEILAALPESAAVRPTC
CRNDDXDERWCYVVKDNALSWEYCRLTACESLARVHSQFPEILAALPESAAVRPTC
GKRHKKRTFLRPRIIGGSSSLPGSHPWLAAIYLGNSFCAGSLVHTCWVVSAAHCFANS
PROSITVVLGQLEFENRTTDVTQTFGLEKYGTAV
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SPEVYGADISPNMLCAGYFDCKSDACQGDSGGPLVCEKNGVAYLYGIISWGDGCGRLN
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/protein_id="AAF34712.1"
/db_xref="GI:6980072"
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/db_xref="taxon:10090"
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Pred. No. 1.8e-27;
0; Mismatches 547;
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Barasch, J.,

HGF in vitro

Biology, NY 10032,

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Mus musculus, clone MGC:30305
BC019376
BC019376.1 GI:18044172
Strausberg, R
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2067)
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5 IMAGE:5134851,
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              CTTTACTGGAACTCCCACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCT
                                              CTGGGAAATGGTACAGAGTACCGAGGCGTGGCCAGCACCGCTGCCTCGGGCCTGAGCTGC
                                                                             GTTGGCGATGGCTACTCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGC
                                                                                                             ACCTGCCCGTTGGGCTATGCTGGGCGGTTCTGTAACATTGTTCCCACAGAGCACTGCTTC
                                                                                                                               GCCTGTCCCGACCAGTTCAAGGGGAAATTCTGTGAAATAGGT---TCTGATGACTGCTAT
                                                                                                                                                                             AGCCCATGTCTGAACGGAGGCACCTGCCACCTGATTGTGGGCACAGGGACCAGCGTCTGC
                                                                                                                                                                                                             AACCCCTGCCAGAATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
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/clone_lib="NCI_CGAP_Li9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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Pred. No. 5.5e-27;
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Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.g. Series: IRAK Plate: 41 Row: o Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 950/Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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OPCREPERY GGRMLHSCTSEGSAV TRKWCATTINY DEDRAKO ZCAEVTLFV EGPALIDP
CASGPCLNGGTCSSTHDHGSY HCSCPLAFTGKDCGTEKCFDETRY EY EF EVEDHMARVS
EGHVEQCGCMEGQARCE DTHHT ACLSSPCLNGGTCHLI VCTGTSVCTCPLGY AGRECN
I VPTEHCFLGNGTEY RGVASTAACISCECLAWNSDLLY QELHVDSVAAAV LLGLGPHAY
CRNPDKDERPWCY VV KDNALSWEYCRLTACESLARVISQS PEI LAALPESAPA VRPTC
GRHKKRTFTERRI I GGSSSLPGSHPWLAAIY I GNGSCAGSLYHTCWV VSAAHCEANS
PRDSITVVLGQHFNRTTIDVTQTFG LERY VPYTLY SVFNENHDLVLIRLKKKGERC
AVRSQFVQPI CLEPAGSSPFTGHKCQLAGWGHMDENVSSY SNSLLEALVPLVADHKCS
                                                                                                                                                                                         SPEYVGADISPNNLCAGYPDCKSDACQGDSGGPLVCEKNGVAYLYGIISWGDGCGRLN
KPGVYIRVANYUDWINDRIRPPKRPVATS"
1 633 C 583 G 418 t
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/protein_id="AAH19376.1"

/db_xref="G:1:8044173"

/translation="MGRQAWISSLCPLPRPCPFLLLLLLLVVPRGAOPQAGRNHTEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="MGC:30305 IMAGE:5134851"
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Martin, R.G., Muzn
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Gaps
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RESI AC1	ду рь	ду рь	Оу	Qy	Qу	Qу	Ор	Оу	Дb	Db	99 V9	Db Qy	ду	ду рь	Оу	Db 04	Db	Db
RESULT 15 AC106236/c	1641 GAATTGGATCAAAGCCACCAT 1661 		1527 TGGAGGCCCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTG 1586	1467 CAGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTC 1526	1407 CAAGCTGATTGCCAACACTTTGTGCAACTCCCGCCAACTCTATGACCACATGATTGAT	1353 CTGGGGTGTTACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGT 1406	1299 TGTGTGCCTGATGGTCCTTTCCCTCTGGGAGTGAGTGCCACATCTCTGG 1352	1339 ATTGCTCAAGTTAAAGCCAGTGGATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGAC 1298 111	GAAGATATTCAAGTACAGCCACTACAATGAAAGAGATGAGATTCCCCACAATGATATTGC	GGTGCTAGGGGACCAGGACCTGAAGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGCA	1065 CTGGGTGCTCACTGCCCACTGCACCCGACATAAAAACCAGACATCTAAAGGT 1118	1005 GCCTCTGACCATCTCCATGCCCCAGGCCACTTCTGTGGTGGGGGGGCTGATCCACCCCTG 1064	945 TGGAGGCTTTAAGAGCACGGGGGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCTCGCT 1004	886 CCGGGGTTTGACTCCTGTGGAAAGACTGAGATAGCAGAGAGAAGATCAAGAGAATCTA- 944		TEGTGCTTTATTAAAGTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCC	GTCCTGCCTGGGCCCTCACGCTTACTGCCGGAACCCAGACAAGGATGAGAGGCCT	922 CTGGCCTGGAATTCTGACCTGCTCTACCAGGAGCTGCACGTGGACTCAGTGGCTGCTGCT 981 706 GAAACCCATGGGATTGGGGAACACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCC 765
	COMMENT	TITLE JOURNAL	REFERENCE	REFERENCE AUTHORS TITLE JOURNAL	TITLE					,					REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	LOCUS:
veb sit	On Jul 11, 2002 this sequence version replaced gi:18138757 Genome Center Center: Baylor College of Medicine Center code: BCM	Direct Submission  Direct Submission  Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 68386) Worley K C	2 (bases 1 to 68586) 2 (bases 1 to 68586) Worley,K.C. Direct Submission Submitsed (12-JAN-2002) Human Genome Sequencing Center. Department	Wu.C., Wu.Y., Wu.Y.F., Zhou,J., Zorfilla,S., Nelson,D., weinstock,G. and Gibbs,R. Direct Submission Unoublished	Tansey, Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliamson, A., Williamson, G., Williamson, A., Williamson, G., Worley K., Washington, C., Worley K., Williamson, G., Worley K., Worley K.	Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stonley, H., Stone, H., Syltton A. Syatek A. Tahor P. Tamerica A. Tahor H.	Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwnonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Pickens,R., Primus,E., Pu.L.,C., Ouiles,M., Ren,Y.,	Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Mahashwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,	Jacobson,B., Jla.Y., Johnson,R., Jolivet,S., Joudah,S., Karisson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H.,	Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,	Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabbisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabbisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,	Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L. D., Dedecth,D.A., Dalaney,K. R. Delagdo O. Denn, A. I. Ding, Y. Dinh H H.	Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buthay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron T. F. Carter M. Cavaros, S. B. Chack, J. Chaver D.	Rattus.  1 (bases 1 to 68586)  1 (bases 1 to 68586)  Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,	ay rat us nor ryota; alia;	9.0	AC106236 68586 bp DNA linear HTG 14-JUL-2002 Rattus norvegicus clone CH230-131J10, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces.

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(see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is
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Center clone name: CH230-131J10
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Search completed: March Job time : 4882 secs

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Listing first 45 summaries
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                                                                                                                                                              Score
        698.2
451.6
447.2
436.2
435.4
435.4
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1: 2: en.
3: en.
4: en.
6: en.
7: em.
7: em.
112: c.
113: c.
113: c.
114: c.
115: c.
116: c.
117: c.
118: c.
118: c.
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119
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US-09-912-559-2
1683
1 atgtttgccaggatgtctga.....aaagtgaaagtggcttctaa 1683
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     3 BI761782
0 BE032018
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AA217892
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## ALIGNMENTS

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FEATURES Source		JOURNAL	AUTHORS TITLE	REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BI761782 LOCUS DEFINITION
http://image.llnl.gov  Plate: LLMM11467 row: e column: 19  High quality sequence stop: 839. Location/Qualifiers 1.891	Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	Onpublished (1999) Contact: Robert Strausberg, Ph.D. Fmail: Contact: Robert Strausberg, Ph.D.	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 891)	81761782 B1761782.1 GI:15753360 EST: Duman.	BI761782 891 bp mRNA linear EST 25-SEP-2001 603046775Fl NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187066 5', mRNA sequence.

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BASE COUNT
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/db_xref="taxon:9606"
/clone="IMAGE:5187066"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
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                                                                                  GCCCTGGTGCTTTATTAAAGTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTC
                            TGCTGAAACCCATGGGATTGGGGAACACAATTTCTGCAGAAACCCAGATGCGGAACAAA 761
                                                                                                                                            CTATGTTGGTGACGGCTACTCTTACCGAGGGGAAGTGAGTAAAAACTGTCAACCAGCACAC 125
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Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST discovery in swine Unpublished (2000) Contact: Smith TPL
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Plate: 69 row: K column: 12
Seg primer: ATTTAGGTCACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                 Library made from pooled tissue and 30 embryos."

152 c 174 q 122 t
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Pred. No. 1.5e-117;
0; Mismatches 69;
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Unpublished (1999)

Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.I.
                                                                                                                                                                                                                                                                                                   Plate: LLAM10967 row: a column: 17
High quality sequence stop: 785.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG972579 802 bp mRNA linear EST 12-JUN-2001
602841165F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4978384
5', mRNA sequence.
BG972579
BG972579.1 GI:14360216
                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM10967 row: a column: 17
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   Conservative
                                                                                 /strain="FVB/N"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="Ib="NCI_CGAP_Kid14"
/clone_lib="NCI_CGAP_Kid14"
/lab_Nost="NCHOBE; Vector: pcMV-SPORT6; Site_1: NotI;
/note="Organ: kidney; Vector: pcMV-SPORT6; Site_1: NotI;
/note="Organ: kidney; Vector: pcMV-SPORT6; Site_1: NotI;
/site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 230 c 203 g 158 t
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                 26.6%;
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   0;
Score 447.2; DB 13;
Pred. No. 3.2e-116;
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RESULT 4 AA217892 LOCUS

AA217892 674 bp mRNA linear EST 06-FEB-199 mv54b08.rl Soares mouse 3NMEL2 5 Mus musculus cDNA clone IMAGE:658839 5′ similar to TR:G1345398 G1345398 HGF ACTIVATOR LIKE

EST 06-FEB-1997

SOURCE ORGANISM

house mouse. Mus musculus

KEYWORDS ACCESSION DEFINITION

EST

PROTEIN. ;, mRNA sequence. AA217892 AA217892.1 GI:1826875

VERSION

REFERENCE

AUTHORS

Eukaryota: Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi; Mammalla; Eutheria: Rodentia; Sciurognathi; Muridae; Mus. Allen, M., Loases I to 674)

1 (bases I to 674)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

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                                              COACCTCTTCTCCAGGAGACTTACAACATGTTTATGGAGGATGCTGAAACCCATGGGAT
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            TGGGGAACACAATTTCTGCAGAAACC 745
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CGCAGAGCACAACTTCTGCAGAAACC
                                                                                                                                                   CAGTATAAGGGGAAATTCTGTGAACATAGGTCCGGACGACTGTTATGTCGGTGATGGCTA
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                                                 CCTGCTGGGTGCTCACTGCTGCCCCCTGCACGACATAAAAACCAGACATCTAAAGGTGG
                                                                                                              CGCTGCCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGCGCTGATCCACC
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TGCTAGGGGACCAGGACCTGAAGAAAGAAGTTTCATGAGCAGAGCTTTAGGGTGCAGA
                                                                                              CACTGCCGTTGACCACCTCCATGCCCCAAGGCCACTTCTGTGGGGGGCGCCCCTGATCCACC
                                                                                                                                                                                                                                                                                                                    CAGCCTGCTCAGCCCAGGACGTTGCCTACCCAGAGGAAAGCCCCCACTGAGCCATCAACCA
                                CCTGCTGGGTGCTCACTGCAGCCCACTGTACCGACATAAACACCAAGCATCTAAAAGTTG
                                                                                                                                                          TCTACGGGGCTTTAAGAGCACAGCAGGCAAGCACCCGTGGCAGGTGTCCCTGCAGACCT
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                                                                                                                                                                                                                                                         AGCTTCCGGGGTTTGACTCCTGTGGAAAGACTGAGATAGCAGAGAGGAGGAAGATCAAGAGAA 940
                                                                                                                                                                                                                                                                                         CAGTCTGTCCAGTGCCTGACACCCCTAACCCAGTGGAAAGCCTTCTGGAGCCTGTGATGG
                                                                                                                                                                                                                                                                                                                                                       AACCCTGGTGTTTCGTCAAGGTGAACAGTGAGAAGGTGAAATGGGAATACTGTGATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:404687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: similarity on ware primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 485.
Location/Qualifiers
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/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
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/clone="IMAGE:658839"
/clone_lib="Soares mouse 3NME12 5"
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/strain="C57BL/6J"
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GTACAGAAACAGG 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://inage.llnl.gov Plate: LLAM11145 row: o column: 08
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I
1 (bases 1 to 751)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D
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602912432F1 NCI_CGAP_Li9
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Tissue Procurement: Jeffrey E. Green,
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                                                                                                                                                                                                                      /clone="IMAGE:5053663"
/clone_lib="NCI_CGAP_Li9"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: Liver; Vector: pcMV-SpORT6; Site_1: Not Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 221 c 188 g 154 t
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                                                                                                                                                                                                                                                                                                                                                                                   /strain="FVB/N"
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BM508620
BM508620.1 GI:18679763
contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Camb
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 570)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hilliter,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T. Jackson,Y. and Bowers,Y.
                                                                                                Unpublished (2000)
Other_ESTs: ii37h03.x1
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                    Institute
Divinity Ave, Cambridge
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCT
                                                                                                                            TCTGGCTGGGGTGTTACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTC 1407
                                                                                                                                                                                                                                                                                                                                             TATGTGAAGACTGTATGTTTGCCCAGCGACCCCTTTCCCTCTGGAACTGAGTGCCACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGATATTGCATTGCTCAAGTTAAAGCCAGTGGATGGTCACTGTGCTCTAGAATCCAAA 1287
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                                                                                              AAGCTAATCGCTAACCCTTTGTGCAACTCCCGACAACTCTATGACCACCACCATCGATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Library was constructed by Dr. Douglas Melton DNA sequencing Washington University Genome Sequencing Center For information obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

134 c 152 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pspORT1; Site_1: Not I; Site_2: Sal I; Five libraries representing EIO.5/12.5 pancreatic bud, EIO.5 pancreas, and adult pancreas, and pancreas, and adult islets of Langerhans were separately constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA was made by oligo-dT priming and size-selected by column
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/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5944156"
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Pred. No. 5.8e-112;
0; Mismatches 85;
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GACTATTACTACAGCTATGAGCAGTCCAGCCCAGACGAAGACCCCAGTGTCACGCAGACC
                           CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACC
                                                          GTCATGGGGCTCTCACTGATGTCCTTCATTGCGCCCCAGACCCAGATNGGACCCCCGAT 163
                                                                           GCCTGTGGGTTCTCCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120
                                                                                                                  ATATTTGTCAGGATGTAGGTGTTCCGTGTCCTGCTAATCGCCCTGGTGGGGAAGTCA 103
                                                                                                                                       ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGGCCCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 929)
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602113411F1 NCI_CGAP_Kid14 Mus
5', mRNA sequence.
BF788188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                            Similarity
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Clone distribution: MGC clone distribution information
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                                                                                                                                                                                                                                                           238
                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 686.
Location/Qualifiers
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                   /Clone="IMAGE:4241642"
/Clone_lib="NCI_CGAP_Kid14"
/Clone_lib="NCI_CGAP_Kid14"
/lab_host="DH1OB (T1 phage-resistant)"
/note="Organ: kidney; Vector: pcMV-SPORT6; Site_1: NotI:
/Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT:
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 275 c 253.g 162 t 1 others
                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
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75.98;
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Pred. No. 2.1e-107;
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                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11328 row: a column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                         quality sequence stop: 787
                        /clone="IMAGE:5133587"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                               /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                              Location/Qualifiers
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
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KEYWORDS
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AA237499
AA237499.1
EST.
house mouse.
       Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vert Eukaryota; Metazoa; Chordata; Craniata; Vert Mammalia; Eutheria; Rodentia; Sciurognathi; 1 (bases 1 to 546)
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musculus cDNA clone IMAGE:679771 5'
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                                     Vertebrata;
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TTTAGGGTGCAGAAGATATTCAAGTACAGCCACTACAATGAAAGAGATGAGATTCCCCAC
                                                                                                                                                            CATCTAAAAGTTGTACTAGGGGATCAGGACCTGAAGAAGACAGAATCCCATGAACAGACC
                                                                                                                                                                                CATCTAAAGGTGGTGCTAGGGGACCAGGACCTGAAGAAGAAGAAGTTTCATGAGCAGAGC
                                                                                                                                                                                                                            GCCCTGATCCACCCCTGCTGGGTGCTCACTGCAGCCCACTGTACCGACATAAACACCAAG
                                                                                                                                                                                                                                                                                                           TCCCTCCAGTCCTCGCTGCCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGG
                                                                                                                                                                                                                                                                                                                                                           GCAGTCAAGCGTATCTACGGGGGGCTTTAAGAGCACAGCAGGCAAGCACCCGTGGCAGGTG
                                                                                                                                                                                                                                                                                           TCCCTGCAGACCTCACTGCCGTTGACCACCTCCATGCCCCAAGGCCACTTCTGTGGGGGC
                                                                                                                                                                                                                                                                                                                                                                             AAGATCAAGAGAATCTATGGAGGCTTTAAGAGCACGGGGGGGCAAGCACCCATGGCAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. L/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thating B. Will Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Possible reversed clone: similarity on wrong seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further MGT:419475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Theising, B., Wylie, T., Lennon, G., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:679771"
/clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e 394.2; Db 2,
J. No. 3.5e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      " JWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 10
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KEYWORDS
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Best Local S
Matches 465
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MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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 181
                             167
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                                            CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGGCTGGGGTGTTACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTC 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATGCTGAGAATCCTGACTGGTACTACACTGAGGGACCAAGCTGATCCATGCCAGCCCAAC
                           CAGTATGAGTACAGCCAAGAGTATAATAACCAGGAAGAGACGCCAGCAGTACCACTGCC 226
                                                                                                                                                                        ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGGCTGGGGGTGTACAGAAACCAGGGAAGGGTTCCGCCAGCTCCTGGATGCTAAAGTC
                                                                                                               GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120
                                                                                                                                            ATGTTTGCCAGAATGTCTGATCTCCATGTTCTGCTGTTAATGGTTCTGGCGGGAAAGACA 106
                                                                                    GCCTTCGGGCTCTCCCTGCTGTTTTCTCACAGAGCCGGACCCAGATTGGACTCCTGAC
                                                                                                                                                                                                     465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV601564
5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5', mRNA sequence.
AV601564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takasuga,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing.
This clone was obtained from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Animal Genetics Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Establishment of a high throughput EST sequencing system poly(A) tail-removed cDNA libraries and determination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Sugimoto,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                  Similarity 81.95; Conservative
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                                                                                                                                                                                                                                                                      /lab_host="DH10B"
/note="Vector: pZL1; Site_1::
was deleted from a Not1 site"
171 c 151 g 135 t
                                                                                                                                                                                                                                                                                                                              /clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="E1KI005A04"
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                      . 608
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                                                                                                                                                                                                                  23.3%;
                                                                                                                                                                                                    0;
                                                                                                                                                                                                  Score 392.6; DB 10; Pred. No. 1.1e-100; 0; Mismatches 97;
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Bos tai
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                                                                                                                                                                                                                                                                                                   Sall; Site_2: Not1;
                                                                                                                                                                                                                                                                         3 others
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cora; Bovoidea;
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
Query Match
Best Local Similarity
Matches 532; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                581
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241 CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGTTCAAGGGGAAATTCTGTGAAATAG 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM9812 row: i column: 23 High quality sequence stop: 717. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
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BE780971 BE780971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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1 (bases 1 to 902)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse
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                                                                                                                                                 223
                                                                                                                                        /clone_lib="NCI_CGAP_Kid14"
/lab_Nost="DH10B (Tl_phage=resistant)"
/lab_Nost="DH10B (Tl_phage=resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
Technologies. Note: this is a NCI_CGAP Library. | "
                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:4223710"
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:12086004
                        23.2%;
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Score 390.4; DB 12;
Pred. No. 5.5e-100;
0; Mismatches 186;
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                                           Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 682)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green,
                                                                                                    house mouse.
Mus musculus
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BI220028.1 GI:14673472
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                                         TCTTACCGAGGGAAAATGAAT-AGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTC
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Plate: LLAM11236 row: i column: 03
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/db_xref="taxon:10090"
/clone="IMAGE:5098442"
/clone=lib="NCI_CGAP_L19"
/lab_bost="DH10B (Tl phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: https://documents.com/primer: Olice Site_2: Salt; Cloned unidirectionally. Primer: Olice Average insert size 1.9 kb. Constructed by Life Average insert size 1.9 kb. Constructed by Li
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| CTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGACCAGTTCAAGGG 551
                                                                                                           GAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCCCACCTCCTCT
                                                                                                                                               GAAATTCTGTGAAATAGGTCCGGACGACTGTTATGTCGGTGATGGCTACTCTTACCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information ca
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5', mRNA sequence.
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Plate: LLAM9855 row: d column:
High quality sequence stop: 625.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia;
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/db_xref="taxon:10090"
/clone="IMAGE:4240465"
/clone=lib="NGI_C6Ap_Kid14"
/lab_host="NGI_C6Ap_Kid14"
/lab_host="DH10B (Tl_phage=resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
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CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACCACTTACC
                               GTCATTGGGCTCTCACTGATGTCCTTCATTGCGCCCCCAGACCCAGANTGCACCCCCCAT 183
                                                  GCCTGTGGGTTCTCCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120
                                                                                                  ATATTTGTCAGGATGTTGGTGTTCCGTGTCCTGCTAATCGCCCTGGTGGGGAAGTCA 123
                                                                                                                     ATGTTTGCCAGGATGTCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCCTGTGGAAAGAC 911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institutes of Health, Mammalian Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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602046804F1 NCI_CGAP_Li9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/clone="IMAGE:4196376"
/clone=Lib="NCI_CGAP_Li9"
/clone_Lib="NCI_CGAP_Li9"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: liver; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP_Library."
a 278 c 260 g 172 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCCGAC
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                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 654)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

The Washd-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 un65h07.yl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:2503549 5' similar to TR:Q14520 Q14520 HGF ACTIVATOR LIKE
PROTEIN: ;, mrna sequence.
                                                                                                                                                                                                          Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW475402.1 GI:7045508
EST.
                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
MGI:1018401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nouse mouse.
                                                                                                               primer: custom primer used
                                                                                            quality sequence stop:
/organism="Mus musculus"
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/db_xref="taxon:10090"
                                                                           Location/Qualifiers
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                                                                                                     CAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC
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TCTTACCGACGCAAAGGGAGTGAGACAGGCAAGCAGAAGCCATGCCT 653
                                                                               CAGGTATAGGGGAAATTCTGTGACATAAGTGCGGACGACTGGTATGTCGGTGATGGCTAC
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                                      TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCT 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer CGACCTGCAGCTCGAGCACA."
193 c 174 g 131 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2503549"
/clone_lib="Sugano mou
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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                 US-08-286-740-1
PCT-US95-09576-1
US-08-811-949-60
US-08-137-116-2
US-08-427-640-7
US-08-811-949-46
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US-08-811-949-52
US-08-811-949-58
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US-08-148-937A-14
US-08-148-910-3
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US-08-148-910-2
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US-08-448-937A-3
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US-08-427-640-3
US-08-427-640-3
US-09-53-498-9
US-09-618-869-9
US-09-813-958-39
US-08-811-949-48
US-08-8813-958-39
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            Patent No. 5344773
Sequence 1, Appli
Sequence 1, Appli
Sequence 60, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 44, Appli
Sequence 46, Appl
Sequence 52, Appli
Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl
Patent No.
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08148910 Patent No. 5466593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2033 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: BUJ.
STREET: Washington
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
7TD: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444403335433228
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-D
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/148, FILING DATE: NO. 5466593ember CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                           IMMEDIATE SOURCE:
   LIBRARY: Pre-made Lambda phage Library,
   LIBRARY: human liver(49, male) cDNA Library (Stratagene)
                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                       NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: 500 Kb Storage
COMPUTER: IBM Compatible
                                                                          ORGANISM:
                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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805 Fifteenth Street, N.W., #700
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2 US-08-811-949-62

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Sequence 10, Appl
Sequence 38, Appl
Sequence 42, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 25, Appl
Patent No. 5200340
Patent No. 5185259
Sequence 3, Appli
Sequence 1, Appli
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Sequence 64, Appl
Sequence 66, Appl
Sequence 50, Appl
Sequence 54, Appl
Sequence 62, Appl
Sequence 62, Appl
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Minimum DB Maximum DB

seq length: 0 seq length: 20

length: 20000000000

Total number

Post-processing:

Minimum Match 0%

Database

Issued\_Patents\_NA:\*

o.

Score

Match

Length

DB

Query

Appli

770.6666222

2033 2033 970 329 329 329 329 11065 11068 11137 1137 1137 11314 11068 11068

Title: Perfect score:

US-09-912-559-2 1683 1 atgtttgccaggat

Scoring table:

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6.8%;

Score 114.4; DB 1 Pred. No. 3.5e-24;

DB 1; Length 2033;

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Query Match
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                                                                                                    TGGGGCCACTTGGATGAGAACGTGAGCGGCTACTCCAGCTCCCTGCGGGAGGCCCTGGTC
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AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCCAGGGTGACTCT 1527
                                                         CCCCTGGTCGCCGACCACAAGTGCAGCCAGCCCTGAGGTCTACGGCGCCGACATCAGCCCC
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                                                                                                                                    ; IMMEDIATE SOURCE:
; LIBRARY: Pre-made Lambda phage Library,
; LIBRARY: human liver(49, male) cDNA Library (Stratagene)
US-08-448-937A-14
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US-08-448-937A-14
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PATENT NO. 5677164
GENERAL INFORMATION:
APPLICANT: Takeshi SHIMOMURA et a
                                                                   Matches
                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: No. 5677164ember 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: 500 Kb Storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
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   742
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                    469 AACCCCTGCCAGAATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGT 528
                                                                                                                                                                                                                                                                        TYPE: nuclei
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/448,937A
FILING DATE: May 24, 1995
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                                                                                      Local
                                                                                                                                                                                                          ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-
SOFTWARE: Wordperfect
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                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                              TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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AGCCCTTGCCTGAACGGGGCACCTGCCACCTGATCGTGGCCACCGGGACCACCGTGTGT 801
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605; Conserv
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                                                                   Conservative
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                                                                  Score 114.4; DB 1;
Pred. No. 3.5e-24;
0; Mismatches 561;
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GGGGGGCCCCTGGCCTGCGAGAAGAACGGCGTGGCTTACCTCTACGGCATCATCAGCTGG
                                                                                                        AACATGCTCTGTGCCGGCTACTT----CGACTGCAAGTCCGACGCCTGCCAGGGGGGACTCA 1794
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                                                                                                                                                                          Matches
                                                                                                                                                                                         Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J
REGISTRATION NUMBER: 33,
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: (FILING DATE: No. 5466 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DO SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
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MEDIUM TYPE: DISKette, 5.25
MEDIUM TYPE: 500 Kb Storage
COMPUTER: IBM Compatible
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LIBRARY: Pre-m
LIBRARY: CDNA
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                                                                               1069
                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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CITY: Washington
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                                                                                                                                                                        Local Similarity 52.7 les 357; Conservative
                                                                                                                                                                                                                                                                                                     ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                              GTGGTGTCGGCCGCCCACTGCTTCTCCCACAGCCCCCCAGGGACAGCGTCTCCGTGGTG
                                                                               GTGCTCACTGCTGCCCACTGCACCGACATAAAAACCAGACA----TCTAAAGGTGGTG 112
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805 Fifteenth Street, N.W.,
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N: 435
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Pred. No. 6.1e-18;
0; Mismatches 290
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RESULT 4
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  APPLICATION NUMBER: 08/148,910
FILING DATE: No. 5677164ember 5, 1993
ATTORNEY_AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-448-937A-3
                                                                                                                                                FILING DATE: May 24,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 5.25 inch, MEDIUM TYPE: 500 Kb Storage COMPUTER: IHM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 805 Fift
CITY: Washington
                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Wenderoth, Lind & Ponack 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
                                                                                                                                                                                        NAY 24, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHIMOMURA et al.
NO. 5677164el Protein and Gene Encoding Said Protein
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Sequence 2, Application US/08148910 Patent No. 5466593
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ORIGINAL SOURCE:
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LENGTH: 970 base pairs
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LIBRARY:
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TELEX:
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                                                                                                              TGGATCAACGACCGGAT
                                                                                                                                                                                GACGGCTGCGGGGGCTCCACAAGCCGGGGGGTCTACACCCGCGTGGCCAACTATGTGGAC
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                                                                                                                                                                                                                                                      GGGCCCCTGGCGAGAAGAACGGCGTGGCTTACCTCTACGGCATCATCAGCTGGGGT
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Pred. No. 6.1e-18;
0; Mismatches 290;
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; LIBRARY: Quick
US-08-148-910-2
               RESULT 6
US-08-148-910-13
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SEQUENCE CHARACTERISTICS:
LENGTH: 329 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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APPLICANT: Takeshi
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                    1381 TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC 1440
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OPERATING SYSTEM: MS-DO
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         1441 CAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                            1561 TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAG-----AAGAGGCCAGGG
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                                                                                                                                                                                                                                                                                                                                                                           52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: 500 Kb Storage
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                                                                                                                                                         AAGTCCGACGCCTGCCAGGGGGGACTCAGGGGGGGCCCCTGGCCTGCGAGAAGAACGGCGTG
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13, Application US/08148910
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805 Fifteenth Street, N.W., #700
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No. 5466593el Protein and Gene Encoding Said Protein
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Pred. No. 5.7e-12;
0; Mismatches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
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; LIBRARY: Quick
US-08-148-910-13
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Best Local Similarity 59.3%;
Matches 163; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 329 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: NO. 546
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Takeshi SHIMOMURA et al. TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding
                                                                                                1561 TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAG-----AAGAGGCCAGGG 1614
                                                                                                                                                                                                                                           1441 CAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT 1500
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                                  1615 GTCTACACCCAAGTTACCAAATTCCTGAATTGGAT 1649
                                                                                                                                                                   1501 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC 1560
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                                                                                                                                                                                                                       112 GAGGTCTACGGCGCCGACATCAGCCCCAACATGCTCTGTGCCGGCTACTT---CGACTGC
289
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MEDIUM TYPE: 500 Kb Storage
COMPUTER: IBM Compatible
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CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                              52 TCCAGCTCCCTGCGGGAGGCCCTGGTCCCCCTGGTCGCCGACCACAAGTGCAGCAGCCCT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                        AAGTCCGACGCCTGCCAGGGGGGACTCAGGGGGGCCCCTGGCCTGCGAGAAGAACGGCGTG
GTCTACACCCGCGTGGCCAACTATGTGGACTGGAT
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                                                                                                                                                                                                                                                                                                                                                                        0;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: NO. 5677164ember 5, ATTORREY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                    1615
                                                                                                                                                                                                                                                                                                      1381 TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC 144C
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ORIGINAL SOURCE:
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LENGTH: 329 base pairs
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MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 500 Kb Storage
                                                                                                                                                                                                                                               1441 CAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAAACCT 1500
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CITY: Washington
                                                                                                                                                                                                                                                                                   52 TCCAGCTCCCTGCGGGAGGCCCTGGTCCCCCTGGTCGCCGACCACAAGTGCAGCAGCCCT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                         TACTACGTCTATGGGATAGTGAGCTGGGGGCCTGGAGTGTGAG-----AAGAGGCCAGGG 1614
GTCTACACCCGCGTGGCCAACTATGTGGACTGGAT 323
                                  GTCTACACCCAAGTTACCAAATTCCTGAATTGGAT 1649
                                                                    GCTTACCTCTACGGCATCATCAGCTGGGGGTGACGGCTGCGGGGCGGCTCCACAAGCCGGGG
                                                                                                                                          AAGTCCGACGCCTGCCAGGGGGACTCAGGGGGGGCCCCTGGCCTGCGAGAAGAACGGCGTG
                                                                                                                                                                           GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC 1560
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805 Fifteenth Street, N.W.,
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IVENTION: No. 5677164el Protein and Gene Encoding Said Protein
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Pred. No. 5.7e-12;
0; Mismatches 103;
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; LIBRARY: Quick-cloneTM human liver cDNA (Clonetech)
US-08-448-937A-13
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                                                                                                                                                                                                                                                                                                                                                              Matches 163;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
NEDIUM TYPE: Diskette, 5.25 in
MEDIUM TYPE: 500 Kb Storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/148,910
FILING DATE: NO. 5677164ember 5
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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                                                                                                                                                                                                                                     1441 CAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT 1500
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LENGTH: 329 base pairs
                   1615 GTCTACACCCAAGTTACCAAATTCCTGAATTGGAT 1649
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ORIGINAL SOURCE:
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CITY: Washington
STATE: D.C.
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GTCTACACCCGCGTGGCCAACTATGTGGACTGGAT
                                                                                                       TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAG-----AAGAGGCCAGGG
                                                                                                                                                             GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAAGGACGGCACC 1560
                                                                       AAGTCCGACGCCTGCCAGGGGGGACTCAGGGGGGGCCCCTGGCCTGCGAGAAGAACGGCGTG 228
                                                                                                                                                                                                                 GAGGTCTACGGCGCCGACATCAGCCCCCAACATGCTCTGTGCCGGCTACTT---CGACTGC
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WENTION: No. 5677164el Protein and Gene Encoding Said
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59.3%;
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Pred. No. 5.7e-12;
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US-08-427-640-1
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Best Local Similarity
Matches 340; Conserv
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FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1088
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
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           1490 TTCAGAAACCTGG---
                                                                                                                                                                                                                                                                        1370 CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT
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TITLE OF INVENTION: Compounds and Methods
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
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TYPE: Nucleic acid
STRANDEDNESS: Double
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                                                                   GCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGACA 865
                                                                                                                 GCAACTCCCCCCCAACTCTATGACCATGATGATGATCATCTATGCAGGAAATC 1489
                                                                                                                                                                                                           CTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCT
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Lilly Corporate Center
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Pred. No. 1.1e-11;
---GCAAGACACCTGCCAGGGTGACTCTGGAGGCC 1534
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US-08-427-640-5
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Best Local Sin
Matches 340;
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/689
FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 5:
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TOPOLOGY: ling
MOLECULE TYPE:
                                                                                                                   1142
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
1202
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NUMBER OF SEQUENCES:
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                                           ACAATGAAAGAGATGAGATTCCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261
                                                                                                                                                                       GCACCGA-----CATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTGA 1141
                          TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATT 625
                                                                                                               AGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCACT 1201
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DEDNESS: double
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Lilly Corporate Center
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Pred. No. 1.1e-11;
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US-08-427-640-3
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Qy
                                                                                                       ; TOPOLOGY: 1; MOLECULE TYPE: US-08-427-640-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08427640 Patent No. 5658788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1490
   1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Berg et al. TITLE OF INVENTION: CC NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1535
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                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/689,410
FILING DATE: 22 APRIL 1991
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pair
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft WC CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1595
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                                                                                                                                                       LENGTH: 1068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Lilly Corpo
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/427,640
                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCAGAAACCTGG-------GCAAGACACCTGCCAGGGTGACTCTGGAGGCC
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   AGGGCCACTTCTGTGGGGGGGGCGCTGATCCACCCCTGCTGGGTGCTCACTGCTGCCCACT 1087
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Lilly Corporate Center
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                     Microsoft Word
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                                                                                                                                                                                                                                             22 APRIL 1991
                                                      4.3%;
50.5%;
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                                                                                                                                                                                                                                                                                                                                                                                      Macintosh
                                       0
                                                    Score 72.2; DB 1;
Pred. No. 1.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                          inch,
                                       Mismatches 288;
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                                                                       Length 1068;
                                       Indels
                                       45;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1137)
US-09-553-498-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                              NUMBER (SEQ ID NO 9
                                                                                                                                                                                                                                         APPLICANT: Ambrosius, Dorothee
APPLICANT: Rudolph, Rainer
APPLICANT: Schaeffner, Joerg
APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: Process for the production
FILE REFERENCE: Case 20379
CURRENT APPLICATION NUMBER: US/09/553,498
CURRENT FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09553498 Patent No. 6309861
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: EP99107412.1 PRIOR FILING DATE: 1999-04-26
                                                                                                           LENGTH: 11
TYPE: DNA
                                                                                                                                                                             NUMBER OF SEQ ID NOS: 10
                                                                                          ORGANISM: E. coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                515 TGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAAT
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Query Match
Best Local Similarity Matches 340;

4.3%; ilarity 50.5%; Conservative

0;

Score 72.2; DB 4; Pred. No. 1.1e-11; 0; Mismatches 288;

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1088 GCACCGA------CATAAAAACCAGACATCTAAAGGTGGTGCTGGGGGGCCCAGGACCTGA 1141
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                                                                                                                                                                            PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR CHAPERONES
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; Sequence 48, Application US/08811949
; Patent No. 5840533
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Best Local Sim
Matches 340;
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1137)
JS-09-618-869-9
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: NASAKI, HITOSHI
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
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TYPE: DNA
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Pred. No. 1.1e-11;
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APPLICANT: RUNCHOLDS, TOTAL CONTROL OF SEA DELICANT: Schaeffner, Joerg APPLICANT: Schaeffner, Joerg APPLICANT: Schaeffner, Joerg APPLICANT: Schaeffner, Joerg Title OF INVENTION: PROCESS FOR THE PRODUCT TITLE OF INVENTION: SECRETED PROTEINS BY CO FILE REFERENCE: 20381
CURRENT APPLICATION NUMBER: US/09/618,869
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR APPLICATION 1000 EP99114811.5
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 9

RESULT 13 US-09-618-869-9

Sequence 9, Application US/09618869 Patent No. 6455279 GENERAL INFORMATION:

APPLICANT:

Ambrosius, Dorthee

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TTCGTGACAACAT 1127

TCAAAGCCACCAT 1661

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; LOCATION:
US-08-811-949-48
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NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-413-3000
TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC con
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                1430
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MOLECULE TYPE:
1052
                                                                                                          1370 CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT 1429
                                                                                                                                                                                                                                                           1142 AGAAAGAAGTTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCACT 1201
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ZIP: 22202
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1755 S. CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 340; Conserv
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GCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGACA 1111
                                  GCAACTCCCGCCAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATC 1489
                                                                        CTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCT
                                                                                                                                              TGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGT
                                                                                                                                                                                                                         CGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACC
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                                                                                                                                                                                                                                                                                                                                                                        TGGTCCCTGGCGAGGAGGAGGAAATTTGAAGTCGAAAATACATTGTCCATAAGGAAT
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05-MAR-1997
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                                                                                                                                                                                 -CTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAA 1369
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Pred. No. 1.2e-11;
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Дd
                                                                                                                                                                                                                  US-08-883-795A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/08883795A Patent No. 5985607
                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1955 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION UNBER: 40,261
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Delcuve, Genev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1292 TTCGTGACAACAT 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1028 AGGGCCACTTCTGTGGTGGGGGGGCGCTGATCCCACCCCTGCTGGTTGCTCACTGCTGCCCACT 1087
                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1649 TCAAAGCCACCAT 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1232 GCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAGGTTACCAACTACCTAGACTGGA 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1595 AGTGTGAGAAGAGG-----CCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGGA 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1172 CCCTGGTGTGTCTGAACGATGGCCGCATCACTTTGGTGGGCATCATCAGCTGGGGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1112 CTCGGAGCGGGGGCCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGCC 1171
1163 GCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGG 1222
                                                                      1103 AGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACT 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-JUN-
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGG 1594
                   GCACCGA-----CATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTGA 1141
                                                                                                                                              340;
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                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                               : (416) 364-7311
(416) 361-1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delcuve, Genevieve
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                             4.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/883,795A
                                                                                                                                            Score 72.2; DB 2;
Pred. No. 1.5e-11;
0; Mismatches 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7841-062
                                                                                                                                                                               Length 1955;
                                                                                                                                              Indels 45;
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1231
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Sez Joj	95 64	g g	B 84	Qy Db	Db Db	дь У	g Qy	Оy	Оy	Qy Db
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me 1 co	1649 1757	1595 1697	1535 1637	1490 1577	1430 1517	1370 1457	1322 1397	1262 1337	1202 1283	1142 1223
Search completed: March 6, 2003, 19:40:23 Job time : 81.5 secs	TCAAAGCCACCAT 1661 	AGTGTGAGAGAGGCCAGGGGTCTACACCCCAAGTTACCAAATTCCTGAATTGGA 1648	CCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGG 1594	TTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCTGGAGGCC 1534	GCAACTCCCGCCAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATC 1489	CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCCAACACTTTGT 1429	TTCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAA 1369	ATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCCT 1321	ACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261	AGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCACT 1201

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Minimum DB
Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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1:
2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478924 seqs, 333959956 residues
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1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 1.0
             /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA: *
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Length	DВ	ID	Description
1	1683	100.0	1683	10	US-09-912-559-2	Sequence 2, Appli
2	1679.8	99.8	1683	10	US-09-912-559-1	1,
ω	1679.8	99.8	3008	10	US-09-880-107-1668	
c 4	120.2	7.1	451	10	US-09-864-761-11164	
c 5	117	7.0	117	10	US-09-864-761-27791	
6	114.4	6.8	2036	10	US-09-954-456-552	
7	114.4	6.8	2036	10	US-09-880-107-1612	1612
8	72.8	4.3	614	10	US-09-879-792-33	
9	72.2	4.3	1689	10	US-09-969-271-6	9
10	72.2	4.3	2519	10	US-09-969-271-5	Sequence 5, Appli
11	72.2	4.3	2641	9	US-09-974-298-144	Sequence 144, App
12	66.4	3.9	1614	10	US-09-888-615-45	
13	66.4	3.9	1748	10	US-09-879-792-11	Sequence 11, Appl
14	66.4	3.9	2412	9	US-09-978-295A-68	Sequence 68, Appl
15	66.4	3.9	2412	9	US-09-978-697-68	-
16	66.4	3.9	2412	9	US-09-978-192A-68	
17	66.4	3.9	2412	9	US-09-999-832A-68	68,
18	66.4	3.9	2412	9	US-09-978-189-68	68,
19	66.4	ω. 9	2412	9	US-10-174-590-63	63,

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	
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- 1	US-10-176-991-63	76-987-		76-750-	76-747-	US-10-176-492-63	US-10-176-488-63	75-743-	- 1	75-739-	74-588-	82-	74-579-	US-10-174-572-63	US-10-173-700-63	US-10-180-557-63	US-10-180-552-63	US-10-176-913-63	L	US-10-176-482-63	2-	80	73-706-	US-10-175-737-63	
	Sequence 63	Sequence 63	Sequence 63	Sequence 63			Sequence 63																Sequence 63	Sequence 63,	
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## ALIGNMENTS

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; TYPE: DNA; ORGANISM: Homo sapiens US-09-912-559-2
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                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/912,559
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: DE 100 36 641.4
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: DE 100 50 040.4
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: DE 100 52 319.6
PRIOR FILING DATE: 2000-10-21
PRIOR APPLICATION NUMBER: DE 101 18 706.8
PRIOR FILING DATE: 2001-04-12
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                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ROEMISCH, JUERGEN
APPLICANT: STOEHR, HANS-ARN
                                                                               Query Match 100.0%; Score 1683; Best Local Similarity 100.0%; Pred. No. 0; Matches 1683; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09912559 Patent No. US20020142316A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MUTH-NAUMANN, GUDRUN
TITLE OF INVENTION: MUTANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
TITLE OF INVENTION: DETECTION METHODS USING SPECIFIC ANTIBODIES
FILE REFERENCE: 06478.1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
WEIMER, THOMAS
BECKER, MARGRET
NERLICH, CLAUDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEUSSNER, ANNETTE
LANG, WIEGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STOEHR, HANS-ARNOLD
                                                                                                                        DB 10;
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                                                                                                                    Length 1683;
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1200	${\tt AAGAAAGAAGTTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCAC}$	1141	Qy
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1140	CCCACTGCACCGACATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG	1081	VQ
1080		1021	Db
1080	TGCCCCAGGGCCACTTCTGTGGTGGGGGCGCTGATCCACCCCTGCTGGGTGCTCACTG	1021	Qy
.02	ACGGCGGCAAGCACCATGGCAGGCGTCCCTCCAGTCCTCGCTGCCTCTGACCATCTCC		Db
0	GGCGGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCTCGCTGCCTCTGACCATCTC	961	Qγ
ō		901	DЬ
960	GTGGAAAGACTGAGATAGCAGAGAGGAAGATCAAGAGAATCTATGGAGGCTTTAAGAG	901	Qy
	GTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCC	841	Db
900	3CCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTTGAC	841	Qy
	GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGAC	781	DЬ
840	CCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAG	781	Qy
780	GGGGAACACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCCCTGGTGCTTTATTAAA	721	Ъ
780	GGGAACACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATT	721	Qy
	CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT	661	Db
720	ACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGG	661	Qy
660	TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC	601	DЪ
660	TTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACI	601	Qy
600	CAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC	541	Db K
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-	ATGGGGCTACCTGCTCCCGGCATAACCCGAGAGCCTTCTACCTGCCCTCTCTCCCCC	481	ν0
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œ	CTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGC	421	Qγ
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Š	GCCGGGGCAATGTCTCATTACCCAGAGTCCTCCTACTACCGCTGTGTCTCTTAAAC	361	Qy
360	GCTCCTTTCTCTGGGAATAAGTGTCAGAAAAGTGCAAAATACGTGCAAGGACAACCCATGT	0	B 4
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240	CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATGCCATGCCAAGCCCAAC	æ	Qy
180	CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACC	121	DЪ
180	AGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAGACACCAGTAGCACACTTAC	121	Qy
		61	Db .
120	CCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTC	61	Qγ

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROEMISCH, JUERGEN
APPLICANT: STOCHR, HANS-ARNOLD
APPLICANT: STOCHR, HANS-ARNOLD
APPLICANT: FEUSSNER, ANNETTE
APPLICANT: HERICAND
APPLICANT: HERICAND
APPLICANT: NERLICH, CLAUDIA
APPLICANT: NERLICH, CLAUDIA
APPLICANT: NERLICH, CLAUDIA
APPLICANT: NERLICH, CLAUDIA
APPLICANT: NUTH-NAUGANN, GUDRUN
TITLE OF INVENTION: MUTANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
TITLE OF INVENTION: MUTANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
TITLE OF INVENTION: MUTANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
TITLE OF INVENTION NUMBER: US/09/912,559
CURRENT APPLICATION NUMBER: US/09/912,559
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: DE 100 36 641.4
PRIOR APPLICATION NUMBER: DE 100 50 040.4
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: DE 100 50 040.4
PRIOR APPLICATION DE 100 100 040.4
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; ORGANISM: Homo sapiens US-09-912-559-1
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; LENGTH: 1683
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Sequence 1668, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: HORDE, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION UMBER: US/09/880,107
CURRENT APPLICATION 1000
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                                                                      PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1668
LENGTH: 30
TYPE: DNA
ORGANISM:
FEATURE:
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                                                  TGTGGAAAGACTGAGATAGCAGAGAGAGAGATCAAGAGAATCTATGGAGGCTTTAAGAGC
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                                                                                      GTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCC
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Conservative
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Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04

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US-09-864-761-11164/c
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Sequence 11164, Application US/09864761

Patent No. US2002048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL:
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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OTHER INFORMATION: MAP TO AC006097.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 1.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 1.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
US-09-864-761-11164
                                                                                                                                US-09-864-761-27791/c

US-09-864-761-27791/, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:
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PRIOR ETLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11164
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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ORGANISM: Homo sapiens
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Matches 117; Conserv
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LENGTH: 117
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APPLICATION NUMBER: PCT/
APPLICATION 2001-01-30
DATE: 2007-01-9CT
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APPLICATION NUMBER: US 09/608,408
ELIPHONE 2000-06-30
ADDITION NUMBER: US 09/608,408
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00666
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                  CTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTCCCAAG
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NN: EXPRESSED IN PLACENTA, SIGNAL = 0.89

NN: EXPRESSED IN LUNG, SIGNAL = 1

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8

NN: EXPRESSED IN BRAIN, SIGNAL = 1.1

NN: EXPRESSED IN BODLE MARROW, SIGNAL = 1.1

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9

NN: WT HIT: S83182.1, EVALUE 8.00e-60

NN: WT SHOTOT HIT: Q25464, EVALUE 7.00e-55
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RESULT 6 US-09-954-456-552; Sequence 552; A

Application US/09954456

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SEQ ID NO 552
LENGTH: 2036
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Best Local
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PRIOR FILING DATE: 2000-09-18
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APPLICATION NUMBER: US/60/235,638
FILING DATE: 2000-09-26
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GGAGGCTTTAAGAGCACGGCGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCTCGCTG 1005
                               CCTGAGCCAGCCTCCCCGGGGGCGCCAGGCCTGCGGCAGGAGGCACCAAGAAGAGGACGTTC
                                                                                      TGCGAATCCCT-----CACCAGAGTCCAACTGTCACCGGATCTCCTGGCGACCCTG
                                                                                                                     TGCTCAGCCCAGGACGTTGCCTACCCAGAGGAAAGCCCCCACTGAGCCATCAACCAAGCTT
                                                                                                                                                                      TGGTGCTTTATTAAAGTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCC
                                                                                                                                                                                                            GCCCTGCTGGGCCTGGGCCCCATGCCTACTGCCGAATCCGGACAATGACGAGAGGCCC
                                                                                                                                                                                                                                                                      CTGGCCTGGAACTCCGATCTGCTCTACCAGGAGCTGCACGTGGACTCCGTGGGCGCCGCG
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                                                         TGGTGCTACGT----GGTGAAGGACAGCGCGCCTCTCCTGGGAGTACTGCCGCCTGGAGGCC
                                                                                                                                                                                                                                       GAAACCCATGGGATTGGGGAACACAATTTCTGCAGAAACCCCAGATGCGGACGAAAAGCCC
                                                                                                                                                                                                                                                                                                     CTTTACTGGAACTCCCACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCT
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05; Conservative
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Pred. No. 7.2e-25;
0; Mismatches 561;
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           SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1612
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US-09-880-107-1612
                                                                                      GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                              Sequence 1612, Application Patent No. US20020142981A1
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.8%;
Best Local Similarity 49.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo :
FEATURE:
    1621
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Best Local Similarity 57.2%;
Matches 175; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/283,648
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 2001-06-12
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CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/211,224
PRIOR FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 60/283,353
PRIOR FILING DATE: 2001-04-13
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SOFTWARE: FastSEQ for
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GTCTACACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGT 167
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Pred. No. 2.9e-12;
0; Mismatches 122;
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; TYPE: DNA
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US-09-969-271-6
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PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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Best Local Similarity 50.5%;
Matches 340; Conservative
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TITLE OF INVENTION: Pharmaceutical Combinations
FILE REFERENCE: PCS10951APME
CURRENT APPLICATION NUMBER: US/09/969,271
CURRENT FILING DATE: 2001-10-01
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                        AGTGTGAGAAGAGG------CCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGGA 1648
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US-09-969-271-5
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APPLICANT: Pfizer Inc. (All designated States except
APPLICANT: Pfizer Limited (GB and EP (GB) only)
TITLE OF INVENTION: Pharmaceutical Combinations
FILE REFERENCE: PCS10951APME
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SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2519
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Best Local Similarity
Matches 340; Conserv
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 0025473.0
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TYPE: DNA
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                                                                                                                                                                            1490 TTCAGAAACCTGG----
                                                                                                                                                                                                                                                                                                                                                  1370 CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT 1429
                                                                                    CCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGG
                                                                                                                                  CTCGGAGCGGCGGCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGCC
                                                                                                                                                                                                                      GCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGACA 1562
                                                                                                                                                                                                                                                                                                          CTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCT
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                                            CCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCCATCATCAGCTGGGGCCTGG
                                                                                                                                                                                                                                                              GCAACTCCCGCCAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATC 1489
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  -- CCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGGA
                                                                                                                                                     -----GCAAGACACCTGCCAGGGTGACTCTGGAGGCC 1534
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Pred. No. 1.1e-11;
0; Mismatches 288;
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US-09-974-298-144
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SOFTWARE: PERL Program
SEQ ID NO 144
LENGTH: 2641
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GENERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
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Best Local Similarity
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TYPE: DNA
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte
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LOCATION: 2635
OTHER INFORMATION: a, t, c, g, or other
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CTCGGAGCGGGGGCCCCAGGCAAACTTGCACGACGCCTGCCAGGGGGGATTCGGGAGGCC 1742
                                          TTCAGAAACCTGG-
                                                                                                                                                 CTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCCAGCCGCT
                                                                                                                                                                                  CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT 1429
                                                                                                                                                                                                                        TGCAGCTGCCGGACTGGACCGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGCCTTGT 1562
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                                                                        GCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCTGGAGACA
                                                                                                             GCAACTCCCGCCAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATC 1489
                                                                                                                                                                                                                                                                       TTCCCT---
                                                                                                                                                                                                                                                                                                                                                                                  TCGAT----
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                                                                                                                                                                                                                                                                                                                                                                            -GATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATT 1442
                                                                                                                                                                                                                                                             -CTGGGAGTGAGTGCCACATCTCTGGCTGGGGGTGTTACAGAAA 1369
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Pred. No. 1.1e-11;
0; Mismatches 288
                                      -GCAAGACACCTGCCAGGGTGACTCTGGAGGCC 1534
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NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-888-615-45
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US-09-888-615-45
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Best Local Similarity
Matches 171; Conserv
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APPLICANT:
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                               1675 GGCTTC 1680
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                                                                                                                                                        1561 TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAGAAGAG------GCCAGGG 1614
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CGATTC 1602
                                                            GTGTACACCAAAGTGACAGAAGTTCTTCCCTGGATTTACAGCAAGATGGAGAGCGAGGTG
                                                                             GTCTACACCCAAGTTACCAAATTCCTGAAGTGGATCAAAGCCACCATCAAAAGTGAAAGT 1674
                                                                                                                                                                                                                                                           TTGGTCTATGACAGTTACCTTACCCCAAGGATGATGTGTGCTGGGGGACCTTCGT----GGG
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                                                                                                                           GGCAGAGACTCCTGCCAGGGAGACAGCGGGGGGGCCTCTTGTCTGTGAGCAGCAGAACAACCGC 1476
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                                                                                                                                                                                                                                                                                                                                                                                            126;
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US-09-879-792-11 Sequence 11, Application US/09879792 Patent No. US20020061850A1 GENERAL INFORMATION:

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; LENGTH: 1748
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-792-11
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CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/211,224
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-04-13
PRIOR PPLICATION NUMBER: US 60/283,353
PRIOR APPLICATION NUMBER: US 60/283,648
PRIOR APPLICATION NUMBER: US 60/283,648
PRIOR APPLICATION NUMBER: US 60/283,648
PRIOR APPLICATION NUMBER: DCT
PRIOR APPLICATION NUMBER: DCT
PRIOR APPLICATION NUMBER: DCT
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FRStSEQ for Windows Version 4.0
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US-09-978-295A-68
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Patent No. US2002015
GENERAL INFORMATION:
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Best Local
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Local Similarity 55.9%;
nes 171; Conservative
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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ed. No. 5.4e-10;
Mismatches 126;
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PRIOR FILING DATE: 1997-11-13
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, Sophia S.
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PRIOR FILING DATE: 1998-03-12  PRIOR APPLICATION NUMBER: 60/078004  PRIOR FILING DATE: 1998-03-13  PRIOR PRIOR APPLICATION NUMBER: 60/078886  PRIOR FILING DATE: 1998-03-20  PRIOR PRIOR DATE: 1998-03-20  PRIOR APPLICATION NUMBER: 60/078910  PRIOR APPLICATION NUMBER: 60/078910  PRIOR PRIOR APPLICATION NUMBER: 60/078939  PRIOR APPLICATION NUMBER: 60/078939  PRIOR FILING DATE: 1998-03-20  PRIOR PRIOR PRICING DATE: 1998-03-25  PRIOR FILING DATE: 1998-03-25  PRIOR APPLICATION NUMBER: 60/079656  PRIOR APPLICATION NUMBER: 60/079664  PRIOR APPLICATION NUMBER: 60/079689  PRIOR PRIOR PRICING DATE: 1998-03-27  PRIOR PRIOR PRICATION NUMBER: 60/079689  PRIOR FILING DATE: 1998-03-27  PRIOR FILING DATE: 1998-03-27  PRIOR APPLICATION NUMBER: 60/079689  PRIOR FILING DATE: 1998-03-27  PRIOR FILING DATE: 1998-03-27  PRIOR PRIOR PRICATION NUMBER: 60/079689  PRIOR FILING DATE: 1998-03-27  PRIOR FILING DATE: 1998-03-27  PRIOR FILING DATE: 1998-03-27  PRIOR FILING DATE: 1998-03-27	TITLE OF INVENTION: Scoreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Scoreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PB1C27 CURRENT APPLICATION NUMBER: US/09/978,697 CURRENT PILING DATE: 2001-07-16 PRIOR APPLICATION NUMBER: 09/91855 PRIOR PILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/064249 PRIOR APPLICATION NUMBER: 60/06434 PRIOR FILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: 60/065364 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: 60/07763 PRIOR APPLICATION NUMBER: 60/07763 PRIOR FILING DATE: 1998-03-11 PRIOR APPLICATION NUMBER: 60/077641 PRIOR APPLICATION NUMBER: 60/0777641	ORMATION: Ashkenazi, Avi Baker Kevin P. Botstein, Davi Desnoyers, Luc Eaton, Dan Ferrara, Napol Filvaroff, Ell Fong, Wei-Qiang Garieritsen, Mar Gerber, Hanspe Gerritsen, Mar Goddard, Audre Goddard, Audre Goddwski, Paul Grinaldi, J. C Gurney, Austin Hillan, Kennett Hillan, Kennett Hillan, Tar Kuo, Sophia S. Napier, Mary & Pan, James; Pan, Ja
PRIOR APPLICATION NUMBER: 09/082790 PRIOR EILING DATE: 1998-04-22 PRIOR APPLICATION NUMBER: 60/082790 PRIOR APPLICATION NUMBER: 60/082797 PRIOR APPLICATION NUMBER: 60/082797 PRIOR APPLICATION NUMBER: 60/082796 PRIOR APPLICATION NUMBER: 60/08336 PRIOR APPLICATION NUMBER: 60/08336 PRIOR APPLICATION NUMBER: 60/083322 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083495 PRIOR APPLICATION NUMBER: 60/083496		PRIOR APPLICATION NUMBER: 60/079728 PRIOR FILING DATE: 1998-03-27 PRIOR APPLICATION NUMBER: 60/079786 PRIOR FILING DATE: 1998-03-20 PRIOR APPLICATION NUMBER: 60/079920 PRIOR APPLICATION NUMBER: 60/079920 PRIOR APPLICATION NUMBER: 60/080105 PRIOR APPLICATION NUMBER: 60/080107 PRIOR APPLICATION NUMBER: 60/080107 PRIOR APPLICATION NUMBER: 60/080107 PRIOR APPLICATION NUMBER: 60/080165 PRIOR APPLICATION NUMBER: 60/080194 PRIOR APPLICATION NUMBER: 60/080194 PRIOR APPLICATION NUMBER: 60/080327 PRIOR APPLICATION NUMBER: 60/080327 PRIOR APPLICATION NUMBER: 60/080327 PRIOR APPLICATION NUMBER: 60/080328 PRIOR APPLICATION NUMBER: 60/080333 PRIOR FILING DATE: 1998-04-01 PRIOR APPLICATION NUMBER: 60/080334 PRIOR APPLICATION NUMBER: 60/08034

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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Ωy В QYВ 40 밁 Qy 망 Qy DЪ Qy DЬ γΩ В δÃ Вb δÃ 뭥 δÃ ₽ QΥ

	TAA 1683	1681	Db
		1681	VQ
1680	. ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC	1621	Db
1680		1621	Qy
1620	TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAGAAGAGGCCAGGGGTCTAC	1561	Qy
1620		1561	Db
1560 1560	GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC		Db Qy
1500 1500	CAACTCTATGACCACATGATTGATGACGAGTATGATCTGTGCAGGAAATCTTCAGAAACCT	1441	Qy Db
1440	TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC	1381	Db
1440		1381	Qy
1380	TTTCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAACAGGAAAAGGG	1321	Db
1380		1321	Qy
1320	GATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCCTGATGGGTCC	1261	Qy
1320		1261	dd
1260 1260	TACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTG	1201 1201	- DA
1200	AAGAAAGAATTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCAC	1141	Db
1200		1141	Db
1140 1140	GCCCACTGCACCGACATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG	1081	dd 40
1080	ATGCCCCAGGGCCACTTCTGTGGTGGGGCCCTGATCCACCCCTGCTGGTGGTGCTCACTGCT	1021	dq
1080		1021	Qy
1020	ACGGCGGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCTCGCTGCCTCTGACCATCTCCCIIIIIIIIII	961	Оу
1020		961	Db
960	TGTGGAAAGACTGAGATAGCAGAGAGAGAGATCAAGAGAATCTATGGAGGCTTTAAGAGC		Oy Db
900	GTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCC	841 841	dd Vo
840	GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGAC	781	Qy
840		781	Db
780	GGGGAACACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAA	721	Qy
780		721	Db
720	CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT	661	Qy
720		661	Db
660	TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC	601	Db

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Best I
                                                                                                                                                                                                                            Matches 1681;
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10-OCT-2000;
21-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a mutant of the DNA sequence encoding the protease (FSAP) that activates blood coagulation factor VII (FVII) and single-chain plasminogen activator, where at least one of the base changes G to C at nucleotide 1177 and G to A at nucleotide 1601 is present. The mutant sequences can be used in the treatment and prevention of bleeding disorders associated with inherited or acquired defects of blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's factor and/or with antibodies against any of these proteins. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roemisch J,
Nerlich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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single-chain
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DB; AAO17144.
    CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACCACCAGTAGCACCTTACC
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                                                                                                                                                                                                                                                  Similarity
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; 2001DE-1018706.
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Muth-Naumann
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/product= "FSAP"
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bleeding disorder; h
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                                                                                                      Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes liver tissue sample
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                                                      Claim
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                                                    CC tumour in a patient, and differentiating metastatic liver cumour in a patient, and differentiating metastatic liver cancer from CC hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a CC tissue sample. The method of the invention has hepatotropic, and CC cytostatic activity. The method is useful for diagnosing and detecting CC the progression of liver cancer, hepatocellular carcinoma and metastatic CC expression profiles which serve as useful diagnostic markers as well as CC expression profiles which serve as useful diagnostic markers as well as CC markers that can be used to monitor disease states, disease progression, CC drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
   Sequence 3008 BP; 791 A; 837
C; 703 G;
   677
T; 0 other;
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QΥ Query Match Best Local Sim Matches 1681; Similarity Conservative 99.8%; 99.9%; Score 1679.8;
Pred. No. 0;
O; Mismatches DB 24; Length 2; Indels 3008; 0; Gaps 0;

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ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60

Matches Query Match

BP;

848 A; 1005 C; 930 G; 840 T; 0

99.5%;

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Pred. No. 0; 0; Mismatches 1675; No. 0

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Length Indels

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cc antipassive antiparkinsonian; nostropic; neuroprotective;
co steopathic; antiparkinsonian; nostropic; neuroprotective;
co steopathic; antiparkinsonian; nostropic; immunosuppressant;
cm antiparkinsonian; thrombolytic; coagulant; vasotropic;
cc antidiabetic; hypotensive; dermatological; immunosuppressive;
cc antihirlammatory; antibacterial; antiviral; antifungal; antirheumatic;
cc antihirproid; and antianaemic. The sequences can be used for determining
cc the presence of or predisposition to, or preventing or treating
cc pathological conditions associated with an OREX-associated disorder. The
cc nucleic acids can be used to express OREX proteins in gene therapy
cc vectors. The proteins and nucleic acids may be used to treat cancers,
cc proliferative disorders, neurodegenerative disorders, osteoarthritis,
cc graft vs host disease, cardiovascular disease, diabetes mellitus,
cc priferative disorders, neurodegenerative disorders, systemic lupus
cc hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
cc erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
cc allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
cc coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antianaemic; gene therapy; cancer; proliferative disorder; hypertensic neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroldism; SCID; AIDS cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma altergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 3679-3681; 5507pp; English.
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                                                                              1680
                                                                                                                                                                                                                1596
                                                                                                                                                                                                                                                                                                                                                                            1416
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AAA44763 standard; cDNA; 617

(first entry)

Human secreted expressed sequence tag SEQ ID NO:1338

RESULT 5
AAA44763
AID AAA44763
AX AAA
XX AAAA
XX AAAA
AX AAAA
AX Human
AX H antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepresant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic; Human; mouse; chicken; rat; secreted expressed sequence tag; expressed sequence tag; EST; probe; chemotactic; proliferation immunomodulatory; haematopoietic; chemokinetic; analgesic; htms. thrombolytic; antiinflammatory; cytostatic; antibacterial; tumour; infection; depression; psoriasis; ss. proliferative; antifungal; haemostatic;

WO200021991-AL

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Qy В QΥ Dр δÃ Dр QΥ DЬ δδ Дb Q DЬ Ş В QY В ΔÃ DЬ Qγ 밁 δÃ Вр Qy B QY В

Вb

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecules which correspond to the SESTS. Proteins encoded by the SESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzhelmer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45931 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective; noctropic; antiparkinsonian; antipsoriatic; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anticonvulsant; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length to DNAs and genomic DNAs and genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tags (SESTs), isolated from human, mouse, chicken and tissue sources. The SESTs can have a range of activities depet the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 549; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317938/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCCAGACTGGACCCCTGAC
GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTGTCTGTAAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGCTGAGAATCCTGACTGGTACTACACTGAGGGACCAAGCTGATCCATGCCAGCCCAAC
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                                                                                                                                                                                                                                                                                                       CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACC
                                                                                                                                                                                GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT
                                                                                                                                                                                                                                                                                                                                                                                                  CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC
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                                                                                                                                     GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to AAA45925 represent specifically claimed tags (sESTs), isolated from human, mouse, of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0104436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 A; 169 C; 148 G; 135 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.3%;
99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 526.4; DB 21
Pred. No. 9.5e-142;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
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ACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAAC 1422

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   Matches
               Query Match
Best Local :
                                                                                          genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57340) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. AB19913 and AB19914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                           Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2002
                                                               Sequence 397
                                                                                                                                                                                                                                                                                               The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular
                                                                                                                                                                                                                                                                                                                                                 Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-034733/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse ischaemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishikawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG
                 Similarity
                                                                                                                                                                                                                                                                                                                                               Page 351-352;
 Conservative
                                                               BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                 103
               14.3%;
                                                               A; 105 C; 111 G; 78
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                                                                                                                                                                                                                                                                                                                                             2690pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related cDNA sequence SEQ ID NO:123
0;
Score 241; DB 24;
Pred. No. 2.6e-59;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΒP
                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagata T,
                                                               T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishii
                            Length 397;
0,
                                                                                                                                                                                                                                                             The method
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ABA58323/c

ID ABA58323 standard; DNA; 451 BI
XX ABA58323;

XC ABA58323;

XX Ol-FEB-2002 (first entry)
XX PT 01-FEB-2002 (first entry)
XX Human foetal liver; gene exp
XX Human; foetal liver; gene exp
XX O9-AUG-2001; 2001WO-US00669.
XX O4-FEB-2000; 2000US-023465.
PR 26-MAY-2000; 2000US-0234697.
PR 30-JUN-2000; 2000US-0334697.
PR 30-JUN-2000; 2000US-0333659.
PR 30-JUN-2000; 2000US-0333659.
PR 30-JUN-2000; 2000US-0333669.
PR 30-JUN-2000; 2000US-033669.
PR 30-JUN-2000; 2000US-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human foctal from the sample of the sample service.
                                                                          probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format dir from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human foetal liver single exon nucleic acid probe #6628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1663 AAAAGTGAAAGTGGCTTCTAA 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTGTGCAACTCCGACAACTCTATGACCACACCATGGATGACAGTATGATTTGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAGGGAGGCTGGCCTCTGA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGAGGCCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATC 1662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGAGAAGGACGGCACCTACCTCTATGGGATAGTGAGCTGGGGCCTGGAGTTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAAGCCAGGAGTCTACACTCAAGTCACCAAGTTCCTGAATTGGATAAAGACCACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGAACCTTCAGAAGCCCGGATCAGACACCTGCCAGGGTGACTCGGGGGGCCCTCTAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome-derived single exon nucleic acid probes useful zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6628; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                          The present sequence is a single exon nucleic acid
             116 A; 102 C; 127 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                           format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1602
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Query Match

Best Local Similarity

7.1%; 97.6%;

Score 120.2; DB 22; Pred. No. 2.4e-24;

451;

Ър

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Qy
                                                                                 RESULT 8
AAK06420/c
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                                                  Query Match
Best Local
                                         Matches
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                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human probes which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                Sequence 451
                                                                                                                                                                                     Example 4;
                                                                                                                                                                                                                     Single
                                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                    04-OCT-2000;
                                                                                                                                                                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human brain expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001
(MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK06420 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGAGTCCTCCCTACCGCTGTGTGTGTAAACACCCTTACACAGGTCCCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122;
                                                                                                                                                                                                                  exon nucleic acid
                                                   Similarity
                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                  SEQ ID NO: 6411; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327
                                                                                                                                                                                                                                                                                                          2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-06323687.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                         Conservative
                                                                                BP; 116 A; 102 C; 127 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                    2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                               2000US-0180312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 451
                                                  7.1%;
97.6%;
                                                                                                                                                                                                                                                          Chen
                                                                                                                                                                                                                  probes
                                                                                                                                                                                                                                                          Σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                  Pred.
                                                            Score 120.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon probe SEQ ID NO:
                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                      No. 2.4e-24;
                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                          Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6411
                                                                                                                                                                                  English
                                       0;
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                                       Gaps
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                                       0;
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9 В 8

В

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RESULT 9
AAK32096/c
ID AAK3200
XX AAK3200
AC AAK320
AC AACA32
AC A
                                                                                                                                                                                                                                                                                    Query Match 7.1%;
Best Local Similarity 97.6%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0532366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-02345359.

04-OCT-2000; 2000US-0234263.
                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 451 BP; 116 A; 102 C; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488900/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK32096 standard; DNA; 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO: 6653; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157276-A2
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                                     444 CCAAG 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384
                                                                             CCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC 443
                                                                                                                                                                                                      TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC 383
                                                                                                                                                                              SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome-derived single exon nucleic acid probes useful
zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone marrow expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US00668
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                                                                                                                                                                                                                                                                            Score 120.2; DB 22; Pred. No. 2.4e-24; Viematches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                  G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                               DB 22; Length 451;
                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                               Gaps
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ABS06863/c
ID ABS0686.
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AC AFF
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Best Local :
        ABS06863;
                                                                                                                                                                                   331
                                                                                                                                                                                                                                                                               391
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                                                                                                                                                                                                                              444 CCAAG
                                                                                                                                                                                                                                                                                                                                  384
                                                                                                                                                                                 CCAAG
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Ş B δÃ В Qy

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RESULT 10
AAI37947/c
ID AAI37947;
XX AAI37947;
XX AAI37947;
XX AAI37947;
XX DE Probe #6633 used to 1
XX Probe: microarray; h
XX Qenetic disorder; ss
XX Probe: microarray; h
XX Qenetic disorder; ss
XX Probe: microarray; h
XX Qenetic disorder; ss
XX Probe: microarray; h
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying ge expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
ABS06863 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 451 BP; 116 A; 102 C; 127 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID No 6633; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00663
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                                                                                                                                                                                                                                                                                                                                                                                        CCAGAGTCCTCCCTACTACCGCTGTGTGTGTAAACACCCCTTACACACGTCCCAGCTGCTC 443
                                                                                                                                                                                                                                                                       CCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; milarity 97.6%; Conservative
                                                                                                                                                                                                               448
                                                                                                                                                           327
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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   451
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ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 120.2; DB 2
Pred. No. 2.4e-24;
0; Mismatches 3
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19-AUG-2002

(first entry)

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CC probes: Also included are a microarray comprising the novel set of concluded are a microarray comprising the novel set of concluded are a microarray comprising the novel set of concluded are a microarray comprising the howel set of concluded acid cacid expression in a cc sample derived from human lung, comprising (a) contacting the array with ca collection of detectably labeled nucleic acids derived from human lung measuring gene expression in a collection and (b) measuring the label detectably bound to each probe of comprising the array identifying exons in a eukaryotic genome, comprising comprising the eukaryote; and (b) detectably by indication of detectably comprise a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising of the expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one cof 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene probes/open analysis, and for identifying exons in a gene, particularly cusing human lung derived mRNA and for the study of lung disease comprised to a linguage comprised expression, period disease, thermalsky-publisk syndrome, servoridates and monomery disease.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary ciliary dyskinesis; pulmonary hypertension;
     Niemann-Pick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spatially-addressable set of single exon nucleic acid probes, used
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; 2000US-207456P.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-234687P.
; 2000US-236359P.
; 2000US-236359P.
; 2000GB-0024263.
disease, Hermansky-Pudlak syndrome, sarcoidosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression in human lung samples
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Best Local
                                                                                                                                                                                                                                                                                   26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertenand hyaline membrane disease. The present sequence is a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the rejector of the sequence data for this patent did not form part.
                                                                                                                                                                                                                                                            21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTACAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC
                                                                                                                            genome-derived single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   foetal liver single exon nucleic acid probe #19224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foetal liver; gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC
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                                                                                                               gene expression in human fetal liver
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-02346359
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2000US-0236359
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                                                                                   IJ
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                                                                                                                                                                                                                                                                                                                                                           2001WO-US00669
                                                                                   NO 19224; 639pp + sequence listing;
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Pred. No. 2.4e-24;
                                                                                                                                                                                      Rank
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                                                                                                                            probes useful
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ARK1917 13
ARAM191 ARK191
AC AAK191
XX 05-NOV
XX DF Human
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Best Local S
Matches 117
                                                                                                                                                                                                                                                                                                                                              04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
27 - SEP - 2000;
04 - OCT - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe of the invention. Note: The sequence data for this patent did not form part of the Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 117
                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK19188 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
                                        Sequence
                                                                                                                                                                                    Example 4;
                                                                                                                                                                                                                  brains
                                                                                                                                                                                                                                                           WPI; 2001-483446/52
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Similarity
                                            117
                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                      SEQ ID NO:
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                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                              2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234685
2000US-0236359
2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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7.0%;
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                                                                                                                                                                                       19179;
                                          24 C;
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                                                                                                                                                                                                                               probes
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Pred. No.
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Score 117;
Pred. No.
                                                                                                                                                                                    650pp + Sequence Listing;
                                          40
                                                                                                                                                                                                                                                                                          Rank
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                                          G;
                                                                                                                                                                                                                                for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe
                                          29 T;
                                                                                                                                                                                                                                                                                          DR
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 DB 22;
1e-23;
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                                            0 other
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RRESULT 14
ARX4513/c
ID ARX451
AC AAK451
AC AAK451
XX O6-NOV
XX Human
XX Human
XX Homo s
XX W02001
XX 09-AUC
XX 09-AUC
XX 09-AUC
XX 07-SEI
PR 26-MAN
PR 26-MAN
PR 27-SEI
PR 04-UCI
PR 01-GEI
PR 04-UCI
PR 04-UCI
PR 07-SEI
PR 04-UCI
PR 07-SEI
PR 04-UCI
PR 04-UCI
PR 07-SEI
PR 07-S
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                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-0207456; 30-JUN-2000; 2000US-0608408; 03-AUG-2000; 2000US-0532366; 21-SEP-2000; 2000US-0234687; 27-SEP-2000; 2000US-0234359; 04-OCT-2000; 2000GB-0024263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK45153;
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                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human bone marrow
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                                                                                                                                                                                                                                                                                           Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO: 19710; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
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                                                 392
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CTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTCCCAAG 448
                                                                                                                       TGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTACCCAGAGTC 391
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                                                                                                TGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTACCCAGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful zing gene expression in human bone marrow - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone marrow expressed exon; gene expression analysis; probe;
rray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                          of the invention.
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                                                                                                                                                                                             Score 117; DB
; Pred. No. 1e-:
0; Mismatches
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RESULT 15
AAI51106/C
ID AAI51106;
XX
AAI51106;
XX
AAI51106;
XX

DT 17-OCT-2001 (first entry)
XX

Probe #19792 used to measure (
XX

Probe; microarray; human; plac
XX

NS

Homo sapiens.

XX

PR

09-AUG-2001; 2000Us-0200663.

PR

20-ANY-2001; 2000Us-0180312.
PR

26-MAY-2000; 2000Us-0180312.
PR

26-MAY-2000; 2000Us-0180312.
PR

27-SEP-2000; 2000Us-053256.
PR

21-SEP-2000; 2000Us-023468.
PR

21-SEP-2000; 2000Us-023468.
PR

21-SEP-2000; 2000Us-023659.
PR

21-SEP-2000; 2000Us-023663.

Search completed: March Job time: 348.5 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 117 BP; 24 A; 24 C; 40 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID No 19792; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                             392 CTCCCTACTACCGCTGTGTCTCTAAACACCCTTACACAGGTCCCAGCTGCTCCCAAG 448
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236559.
2000US-0236559.
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                                  2003, 16:01:40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 117;
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